

SEARCH REQUEST FORM

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Requester's Full Name: _____ Examiner #: _____ Date: _____
 Art Unit: _____ Phone Number 30 _____ Serial Number: _____
 Mail Box and Bldg/Room Location: _____ Results Format Preferred (circle): PAPER DISK E-MAIL

If more than one search is submitted, please prioritize searches in order of need.

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc, if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: _____

Inventors (please provide full names): _____

Earliest Priority Filing Date: _____

**For Sequence Searches Only* Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.*

STAFF USE ONLY

	Type of Search	Vendors and cost where applicable
Searcher: _____	NA Sequence (#) _____	STN _____
Searcher Phone #: _____	AA Sequence (#) _____	Dialog _____
Searcher Location: _____	Structure (#) _____	Questel/Orbit _____
Date Searcher Picked Up: _____	Bibliographic _____	Dr. Link _____
Date Completed: <u>4/10</u>	Litigation _____	Lexis/Nexis _____
Searcher Prep & Review Time: _____	Fulltext _____	Sequence Systems _____
Clerical Prep Time: _____	Patent Family _____	WWW/Internet _____
Online Time: _____	Other _____	Other (specify) _____

GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: April 10, 2003, 11:52:51 ; Search time 30 Seconds
(Without alignments) 1428.593 Million cell updates/sec

Title: US-09-720-469A-44

Perfect score: 208

Sequence: 1 MKVLAAALINGSVFLLLP.....VIIADCGKIEVEKPPAIAKE 208

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 671580 seqs, 206047115 residues

Word size : 0

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

SPTREMBL_21:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phase:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp Vertebrate:*
14: sp Unclassified:*
15: sp_Virus:*
16: sp_Bacteriap:*
17: sp_Archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	208	100.0	216	4 Q9BVK5	Q9BVK5 homo sapien
2	98	47.1	208	11 Q8B541	Q8B541 ratius norv
3	98	47.1	216	11 Q9DCY1	Q9DCY1 mus musculu
4	37	17.8	203	3 Q01490	Q01490 orpilmoyces
5	29	13.9	212	3 Q8X166	Q8X166 aspergillus
6	28	13.5	87	6 Q29278	Q29278 sus scrofa
7	28	13.5	214	3 Q94190	Q94190 emericella
8	19	9.1	162	10 Q92P54	Q92P54 griffithsia
9	19	9.1	207	3 Q8X0S3	Q8X0S3 neurospora
10	18	8.7	120	5 Q91V73	Q91V73 dirosophila
11	18	8.7	143	5 Q25093	Q25093 hirufo medl
12	18	8.7	205	5 Q9W227	Q9W227 dirosophila
13	18	8.7	220	5 Q44073	Q44073 tachypneus
14	18	8.7	226	3 Q93826	Q93826 arthroderna
15	17	8.2	167	5 Q15729	Q15729 entamoeba h
16	17	8.2	204	5 Q62190	Q62190 caenorhabdi

17	16	7.7	197	5 Q9TW32	Q9TW32 dictyosteli
18	16	7.7	212	4 Q96CA2	Q96CA2 homo sapien
19	16	7.7	213	5 Q27774	Q27774 schistosoma
20	15	7.2	173	10 Q9FW22	Q9FW22 oryza sativ
21	15	7.2	177	4 Q43447	Q43447 homo sapien
22	15	7.2	177	11 Q9CQ07	Q9CQ07 mus musculu
23	15	7.2	183	5 Q9V9B9	Q9V9B9 dirosophila
24	15	7.2	188	11 Q9D868	Q9D868 mus musculu
25	15	7.2	210	5 Q9U6U5	Q9U6U5 plasmodium
26	15	7.2	210	5 Q27716	Q27716 plasmodium
27	14	6.7	172	10 Q65104	Q65104 chlamydomon
28	14	6.7	213	5 Q26551	Q26551 schistosoma
29	13	6.2	87	11 Q9QWD4	Q9QWD4 ratius sp.
30	13	6.2	104	13 Q98UE5	Q98UE5 xenopus lae
31	13	6.2	165	3 Q9HPU2	Q9HPU2 magnaporthe
32	13	6.2	172	10 Q96417	Q96417 digitalis l
33	13	6.2	179	5 Q26994	Q26994 toxoplasma
34	13	6.2	215	3 Q9HFU3	Q9HFU3 magnaporthe
35	13	6.2	234	10 Q9LY53	Q9LY53 arabidopsis
36	13	6.2	357	4 Q96D99	Q96D99 homo sapien
37	13	6.2	752	11 Q55035	Q55035 ratius norv
38	13	6.2	754	4 Q13427	Q13427 homo sapien
39	12	5.8	105	4 Q9BVG1	Q9BVG1 homo sapien
40	12	5.8	112	10 Q65191	Q65191 ficus distl
41	12	5.8	156	6 Q9M2D3	Q9M2D3 canis famli
42	12	5.8	160	10 Q9W530	Q9W530 euphorbia e
43	12	5.8	161	5 Q26565	Q26565 schistosoma
44	12	5.8	164	5 Q9X225	Q9X225 lumbricus r
45	12	5.8	164	11 Q9CWJ5	Q9CWJ5 mus musculu

ALIGNMENTS

RESULT 1

Q9BVK5; ID Q9BVK5; PRELIMINARY; PRT; 216 AA.
AC Q9BVK5;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Peptidylprolyl isomerase B (cyclophilin B).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=SKIN;
RA Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=SKIN;
RA Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=PROSTATE;
RA Strausberg R.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: PPIASES ACCELERATE THE FOLDING OF PROTEINS (BY SIMILARITY).
CC -!- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC PEPTIDE BONDS IN OLIGOPEPTIDES.
CC -!- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY.
DR EMBL: BC001125; AAH01125.1; -;
DR EMBL: BC008848; AAH08848.1; -;
DR EMBL: BC020800; AAH20800.1; -;
DR HSSP: P23284; ICYN.
DR InterPro: IPR002130; CSA_PPIase.
DR Pfam: PF00160; pro_isomerase; 1.
DR PRINTS: PR00153; CSA_PPIASE.

DR PROSITE: PS00170; CSA_PPIASE_1; 1.
 DR PROSITE: PS30072; CSA_PPIASE_2; 1.
 KW Isomerase; Rotamase.
 SO SEQUENCE 216 AA; 23742 MW; 2D0410A07AA9E420 CRC64;
 Query Match 100.0%; Score 208; DB 4; Length 216;
 Best Local Similarity 100.0%; Pred. No. 1,5e-204;
 Matches 208; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MKVLLAAALAGSVFLLPLPGPSADDEKKRKPKYVYKFDLRICDEVDGVRVIGLQKGT 60
 DB 9 MKVLLAAALAGSVFLLPLPGPSADDEKKRKPKYVYKFDLRICDEVDGVRVIGLQKGT 68
 OY 61 VPKTVDFVALATGEGFGYKNSKFRHVIKDFMIOGGDPTRGDGTGSKSIYGERPPDENF 120
 DB 69 VPKTVDFVALATGEGFGYKNSKFRHVIKDFMIOGGDPTRGDGTGSKSIYGERPPDENF 128
 OY 121 KLKHYGGMVSMANAGKDTNGSOFITTYKTATMDGKRVYSEKVEEGEYVRYKVESTKTD 180
 DB 129 KLKHYGGMVSMANAGKDTNGSOFITTYKTATMDGKRVYSEKVEEGEYVRYKVESTKTD 188
 OY 181 SRDKPLKDVIIADCGKIEVEKPPAIAKE 208
 DB 189 SRDKPLKDVIIADCGKIEVEKPPAIAKE 216

RESULT 2
 ID 088541 PRELIMINARY; PRT; 208 AA.
 AC 088541;
 DT 01-NOV-1998 (TReMBLrel. 08, Created)
 DT 01-NOV-1998 (TReMBLrel. 08, Last sequence update)
 DT 01-MAR-2002 (TReMBLrel. 20, Last annotation update)
 DE Cyclophilin B
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Wistar-Kyoto; TISSUE=KIDNEY;
 RA Kainer D.B., Doris P.A.;
 RT "Cyclophilin B";
 RL Submitted (JUN-1998) to the EMBL/Genbank/DBJ databases.
 CC -1- FUNCTION: PPIASES ACCELERATE THE FOLDING OF PROTEINS (BY SIMILARITY).
 CC -1- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC PEPTIDE BONDS IN OLIGOPEPTIDES.
 CC -1- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY.
 DR EMBL: AF071225; AAC25590.1; -;
 DR HSSP: P23284; ICYN;
 DR InterPro: IPR002130; CSA_PPIase.
 DR Pfam: PF00160; Pro_Isoomerase; 1.
 DR PRINTS: PR00153; CSAPPISMRASE.
 DR PROSITE: PS00170; CSA_PPIASE_1; 1.
 DR PROSITE: PS30072; CSA_PPIASE_2; 1.
 KW Isomerase; Rotamase.
 SO SEQUENCE 208 AA; 22802 MW; 0240BDFA7157218C CRC64;

Query Match 47.1%; Score 98; DB 11; Length 208;
 Best Local Similarity 100.0%; Pred. No. 6,4e-92;
 Matches 98; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 54 FGLGKTVPTVDNFVALATGEGFGYKNSKFRHVIKDFMIOGGDPTRGDGTGSKSIYGE 113
 DB 54 FGLGKTVPTVDNFVALATGEGFGYKNSKFRHVIKDFMIOGGDPTRGDGTGSKSIYGE 113
 OY 114 RPPDENFKLKHYGGMVSMANAGKDTNGSOFITTYKT 151
 DB 114 RPPDENFKLKHYGGMVSMANAGKDTNGSOFITTYKT 151

RESULT 3

O9DCY1
 ID O9DCY1 PRELIMINARY; PRT; 216 AA.
 AC O9DCY1;
 DT 01-JUN-2001 (TReMBLrel. 17, Created)
 DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
 DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
 DE Peptidylprolyl isomerase B.
 GN PPIB.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=KIDNEY;
 RX MEDLINE=21085660; PubMed=11217651;
 RA Kawai Y., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arikawa T., Hara A., Fukunishi Y., Kono H., Aachli J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Schriml L.M., Staudli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsi G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata S., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weltz C., Whitaker C., Wilming L.,
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kontaaki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=BREAST TUMOR;
 RA Strausberg R.;
 RL Submitted (AUG-2001) to the EMBL/Genbank/DBJ databases.
 DR EMBL: AK001357; BAB22036.1; -;
 DR EMBL: BC013061; AAH13061.1; -;
 DR HSSP: P23284; ICYN;
 DR MGD: MGI:97750; Ppib.
 DR InterPro: IPR002130; CSA_PPIase.
 DR Pfam: PF00160; Pro_Isoomerase; 1.
 DR PRINTS: PR00153; CSAPPISMRASE.
 DR PROSITE: PS00170; CSA_PPIASE_1; 1.
 DR PROSITE: PS30072; CSA_PPIASE_2; 1.
 KW Isomerase.
 SO SEQUENCE 216 AA; 23713 MW; CE9DAD1544AE72FE CRC64;

Query Match 47.1%; Score 98; DB 11; Length 216;
 Best Local Similarity 100.0%; Pred. No. 6,6e-92;
 Matches 98; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 54 FGLGKTVPTVDNFVALATGEGFGYKNSKFRHVIKDFMIOGGDPTRGDGTGSKSIYGE 113
 DB 62 FGLGKTVPTVDNFVALATGEGFGYKNSKFRHVIKDFMIOGGDPTRGDGTGSKSIYGE 121
 OY 114 RPPDENFKLKHYGGMVSMANAGKDTNGSOFITTYKT 151
 DB 122 RPPDENFKLKHYGGMVSMANAGKDTNGSOFITTYKT 159

RESULT 4
 ID 001490 PRELIMINARY; PRT; 203 AA.
 AC 001490;
 DT 01-NOV-1998 (TReMBLrel. 08, Created)
 DT 01-NOV-1998 (TReMBLrel. 08, Last sequence update)
 DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)

DE Peptidyl-prolyl cis-trans isomerase B precursor (EC 5.2.1.8) (PPIase)
 DE (Cyclophilin B) (Rotamase).
 GN CYPB.
 OS Orpinomyces sp. PC-2.
 OC Eukaryota; Fungi; Chytridiomycota; Neocallimastixales;
 CC Neocallimastixaceae; Orpinomyces.
 NC NCBL_TaxID=50059;
 RN (1)
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 23-52.
 RX MEDLINE=9523986; PubMed=7708690;
 RA Chen H., Li X.-L., Ljungdahl L.G.;
 RT "A cyclophilin from the polycentric anaerobic rumen fungus Orpinomyces
 RT sp. strain PC-2 is highly homologous to vertebrate cyclophilin B.*";
 RL Proc. Natl. Acad. Sci. U.S.A. 92:2587-2591(1995).
 CC -1- FUNCTION: PHASES ACCELERATE THE FOLDING OF PROTEINS.
 CC -1- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC
 CC PEPTIDE BONDS IN OLIGOPEPTIDES.
 CC -1- ENZYME REGULATION: CYCLOSPORIN A (CSA) INHIBITS CYPB.
 CC -1- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM LUMEN (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY.
 DR EMBL: U17900; AAD04195.1; -.
 DR HSP: P23284; ICYN
 DR Interpro: IPR002130; CSA_PPIase.
 DR Pfam: PF00160; pro_isomerase; 1.
 DR PRINTS: PR00153; CSA_PPIASMRASE.
 DR PROSITE: PS00170; CSA_PPIASE_1; 1.
 DR PROSITE: PS0072; CSA_PPIASE_2; 1.
 KW isomerase; Rotamase; Signal; Cyclosporin; Endoplasmic reticulum.
 FT SIGNAL 1 22
 FT CHAIN 23 203 PEPTIDYL-PROXYL CIS-TRANS ISOMERASE B.
 FT BINDING 147 147 CSA (POTENTIAL).
 FT SITE 200 203 PREVENT SECRETION FROM ER
 FT (BY SIMILARITY).
 SQ SEQUENCE 203 AA; 21969 MW; A5748C94305B8BE0 CRC64;
 Query Match 17.8%; Score 37; DB 3; Length 203;
 Best Local Similarity 100.0%; Pred. No. 1.8e-29;
 Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 79 GYKNSKFRVHYKDFPMIOGDFTRGDTGKSTYGERF 115
 DB 73 GYKNSKFRVHYKDFPMIOGDFTRGDTGKSTYGERF 109
 RESULT 5
 ID 08X166 PRELIMINARY; PRT; 212 AA.
 AC 08X166;
 DT 01-MAR-2002 (TREMBlrel. 20, Created)
 DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE Cyclophilin-like peptidyl prolyl cis-trans isomerase (EC
 DE 5.2.1.8).
 GN CYPB.
 OS Aspergillus niger.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
 CC Eurotiiales; Trichocomaceae; Mitosporic Trichocomaceae; Aspergillus.
 NC NCBL_TaxID=5061;
 RN (1)
 RP SEQUENCE FROM N.A.
 RA Derix P.M.F., Madrid S.M.;
 RT "The foldase CYPB is a component of the secretory pathway of
 RT Aspergillus niger and contains the endoplasmic reticulum retention
 RT signal HDEL.";
 RL Mol. Gen. Genet. 266:537-545(2001).
 DR EMBL: AT003867; AAF96447.1; -.
 DR Interpro: IPR002130; CSA_PPIase.
 DR Pfam: PF00160; pro_isomerase; 1.
 DR PRINTS: PR00153; CSA_PPIASMRASE.
 DR PROSITE: PS00170; CSA_PPIASE_1; UNKNOWN_1.
 DR PROSITE: PS0072; CSA_PPIASE_2; 1.
 DR PROSITE: PS00014; ER_TARGET; UNKNOWN_1.

KW Isomerase.
 SQ SEQUENCE 212 AA; 23302 MW; FA00BA7D1E50019C CRC64;
 Query Match 13.9%; Score 29; DB 3; Length 212;
 Best Local Similarity 100.0%; Pred. No. 3e-21;
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 65 FHRVYKDFPMIOGDFTRGDTGKSTYGE 113
 DB 64 FHRVYKDFPMIOGDFTRGDTGKSTYGE 112
 RESULT 6
 ID 029278 PRELIMINARY; PRT; 87 AA.
 AC 029278;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE Cyclophilin B (Fragment).
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.
 NC NCBL_TaxID=9823;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC TISSUE=SMALL INTESTINE;
 RX MEDLINE=96327607; PubMed=8672129;
 RA Winteroe A.K., Fredholm M., Davies W.;
 RT "Evaluation and characterization of a porcine small intestine cDNA
 RT library.";
 RL Mamm. Genome 7:509-517(1996).
 DR EMBL: F14628; CA23162.1; -.
 DR HSP: P23284; ICYN.
 DR Interpro: IPR002130; CSA_PPIase.
 DR Pfam: PF00160; pro_isomerase; 1.
 DR PRINTS: PR00153; CSA_PPIASMRASE.
 DR PROSITE: PS0072; CSA_PPIASE_2; 1.
 FT NON_TER 1 1
 FT NON_TER 87 87
 SQ SEQUENCE 87 AA; 9551 MW; EB3EAE8ED630AE97 CRC64;
 Query Match 13.5%; Score 28; DB 6; Length 87;
 Best Local Similarity 100.0%; Pred. No. 1.3e-20;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 153 WLDGKHVYGVKYLEGMEVYRRVSTKTD 180
 DB 32 WLDGKHVYGVKYLEGMEVYRRVSTKTD 59
 RESULT 7
 ID 094190 PRELIMINARY; PRT; 214 AA.
 AC 094190;
 DT 01-MAY-1999 (TREMBlrel. 10, Created)
 DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
 DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
 DE Cyclophilin B.
 GN CYPB.
 OS Emeritella nidulans.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
 CC Eurotiiales; Trichocomaceae; Emeritella.
 NC NCBL_TaxID=162425;
 RN (1)
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99343878; PubMed=10413615;
 RA Joseph J.D., Hellman J., Means A.R.;
 RT "Molecular cloning and characterization of Aspergillus nidulans
 RT cyclophilin B.";
 RL Fungal Genet. Biol. 27:55-66(1999).
 CC -1- FUNCTION: PPIASES ACCELERATE THE FOLDING OF PROTEINS (BY
 CC SIMILARITY).

RESULT 9	
ID	PRELIMINARY:
08X053	PRT: 207 AA.
08X053	
01-MAR-2002 (TEMBUREl. 20, Created)	
01-MAR-2002 (TEMBUREl. 20, Last sequence update)	

	RESULT	10		
	Q917V3			
ID	Q917V3	PRELIMINARY:	PRF:	120 AA.
AC	Q917V3;			
DT	01-MAR-2001 (TREMBLrel. 16, Created)			
DT	01-MAR-2001 (TREMBLrel. 16, Last sequence update)			
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)			
DE	CG2852 protein.			
GN	CG2852.			
OS	Drosophila melanogaster (fruit fly).			
OC	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;			
OC	Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;			
OC	Ephydroidea; Drosophilidae; Drosophila.			
OX	NCBI_TaxID=7227;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN-BERKELEY:			
RX	MEDLINE=201956006; PubMed=10731132;			
RA	Adams M.D., Celisnker S.E., Holt R.A., Evans C.A., Gocayne J.D.,			
RA	Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.S.N.,			
RA	George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,			
RA	Sutton G.C., Morten J.R., Yendell M.D., Zhang Q., Chen L.X.,			
RA	Brandon R.C., Rogers Y.-H.C., Blazel R.G., Champs M., Pfeiffer B.D.,			
RA	Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,			
RA	Abbil J.F., Agbayanti A., An H.-U., Andrews-Pfannkuch C., Baldwin D.,			
RA	Baillet R.M., Basu A.B., Bakendale J., Bayraktaroglu L., Beasley E.M.,			
RA	Beeson K.Y., Benos P.V., Bernan B.P., Bhargava D., Bolshakov S.,			
RA	Botvina D., Botchan M.R., Bouck J., Brokstein P., Broctier P.,			
RA	Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,			
RA	Cherry J.M., Cavley S., Dahle C., Daventport L.B., Davies P.,			
RA	de Pablos B., Delcher A., Deng Z., Mayas A.D., Dew I., Dietz S.M.,			
RA	Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,			
RA	Dutdin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,			
RA	Foster C., Gabriellian A.E., Gar H.N., Gelbart W.M., Glaeser K.,			
RA	Glocke A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,			
RA	Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,			
RA	Hoslin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwan C.,			
RA	Jalali M., Kalush F., Kapten G.H., Ke Z., Kennison J.A., Ketchum K.A.,			
RA	Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai X.,			
RA	Lasto P., Leay V., Levitsky A.A., Liu J., Li Z., Ling Y., Lin Z.,			

RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry G., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacleb J.M.,
 RA Palazzolo M., Pittman K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Reinert K., Remington K., Simpson M., Skupski M.P., Smith T.,
 RA Shue B.C., Spadling A.C., Stapleton M., Strong R., Sun E.,
 RA Spier E., Spradling A.C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Svirska R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodard T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhao M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
 RA "The genome sequence of Drosophila melanogaster";
 RL Science 287:2185-2195(2000).
 DR EMBL: AE003458; AAC22196.1; .
 DR HSSP: P23284; 1CYN.
 DR FLYBASE: FBgn0034753; CG2852.
 DR InterPro: IPR002130; CSA_PPIase.
 DR Pfam: PF00160; PRO_IsoMerase_1.
 DR PRINTS: PR00153; CSA_PPI_MKASE.
 DR PROSITE: PS50072; CSA_PPIASE_2; 1.
 SQ SEQUENCE 120 AA; 12962 MW; CF93898B694F89F8 CRC64;

Query Match 8.7%; Score 18; DB 5; Length 120;
 Best Local Similarity 100.0%; Pred. No. 3, 2e-10;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 131 SWANNGKPTNGSOFFITTT 148
 DB 39 SWANNGKPTNGSOFFITTT 56

RESULT 11
 ID 025093 PRELIMINARY; PRT; 143 AA.
 AC 025093;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DE Cyclophilin-A.
 GN Hcyp.
 OS Hirudo medicinalis (Medicinal leech).
 OC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinea; Hirudinea;
 OC Arynchobdellida; Hirudiniiformes; Hirudiniidae; Hirudo.
 OX NCBI_TaxID=6421;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE-96165729; PubMed-8597897;
 RA Korneev S., Blackshaw S.E., Kaiser K., Davies J.A.;
 RT "CDNA libraries from identified neurons.";
 RL Proc. R. Soc. Lond., B, Biol. Sci. 263:57-62(1996).
 CC -1- FUNCTION: PPIASES ACCELERATE THE FOLDING OF PROTEINS (BY
 CC SIMILARITY).
 CC -1- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC
 CC PEPTIDE BONDS IN OLIGOPEPTIDES.
 CC -1- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY.
 DR EMBL: U06797; AB01531.1; .
 DR HSSP: P05092; 2CPL.
 DR InterPro: IPR002130; CSA_PPIase.
 DR Pfam: PF00160; pro_IsoMerase_1.
 DR PRINTS: PR00153; CSA_PPI_MKASE.
 DR PROSITE: PS00170; CSA_PPIASE_1; 1.
 DR PROSITE: PS50072; CSA_PPIASE_2; 1.
 KW IsoMerase; Rotamase.
 SQ SEQUENCE 143 AA; 15398 MW; 64FFD82018480A6B CRC64;

Query Match 8.7%; Score 18; DB 5; Length 143;
 Best Local Similarity 100.0%; Pred. No. 3, 8e-10;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 95 QGDFTRGDGTGKSIYIG 112

DB 42 QGDFTRGDGTGKSIYIG 59

RESULT 12
 ID 09W227 PRELIMINARY; PRT; 205 AA.
 AC 09W227;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DE CG2852 protein.
 GN CG2852.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachyera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BERKELEY;
 RX MEDLINE-20196006; PubMed-10731132;
 RA Adams M.D., Celisner S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Fandel M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Hele J., Nelson C.R., Mikos G.L.G.,
 RA Abail J.F., Aghayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borokova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.P., Dew I., Dietz S.M.,
 RA Dodson K., Dou P.L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Foster C., Gabrielian A.E., Gary N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibeigbam C.,
 RA Jajani M., Kalush C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Laske P., Lei Y., Levitsky A.A., Li J., Li Z., Liang X., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry G., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacleb J.M.,
 RA Palazzolo M., Pittman K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Reinert K., Remington K., Simpson M., Skupski M.P., Smith T.,
 RA Shue B.C., Spadling A.C., Stapleton M., Strong R., Sun E.,
 RA Spier E., Spradling A.C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Svirska R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodard T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhao M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster";
 RL Science 287:2185-2195(2000).
 CC -1- FUNCTION: PPIASES ACCELERATE THE FOLDING OF PROTEINS (BY
 CC SIMILARITY).
 CC -1- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC
 CC PEPTIDE BONDS IN OLIGOPEPTIDES.
 CC -1- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY.
 DR EMBL: AE003458; AAF46873.1; .
 DR HSSP: P23284; 1CYN.
 DR FLYBASE: FBgn0034753; CG2852.
 DR InterPro: IPR002130; CSA_PPIase.
 DR Pfam: PF00160; pro_IsoMerase_1.
 DR PRINTS: PR00153; CSA_PPI_MKASE.
 DR PROSITE: PS00170; CSA_PPIASE_1; 1.
 DR PROSITE: PS50072; CSA_PPIASE_2; 1.

Db |||||
55 FHRV1KDFM10GDBFTR 71

Search completed: April 10, 2003, 11:55:13
Job time : 33 secs

GenCore version 5.1.4-p5-4578
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OM protein - protein search, using sw model

Run on: April 10, 2003, 11:51:46 ; Search time 36 Seconds

(without alignments)
769,892 Million cell updates/sec

Title: US-09-720-469a-44

Sequence: 1 MKVLAAALTAGSVFFLLP.....VIADCGKIEVKEPFAAKE 208

Scoring table: OLIGO

Gapop 60.0 , Gapept 60.0

Searched: 908470 seqs, 133250620 residues

Word size : 0

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

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20: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.*
21: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
22: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
23: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	208	100.0	22 AAB73301	Human cyclophilin
2	208	100.0	291 21 AAB43878	Human cancer assoc
3	208	100.0	291 23 ABA41842	Human ovarian anti
4	203	97.6	211 22 AAB73302	Human cyclophilin
5	183	88.0	183 22 AAG65273	Haematopoietic site
6	137	65.9	166 21 AAG00090	Haematopoietic site
7	98	47.1	183 22 AAG65274	Human secreted pro
8	64	30.8	63 23 AAG09181	Haematopoietic site
9	29	13.9	212 21 AAY92048	Partial human pert
10	22	10.6	83 22 AAM24287	A. niger peptidyl- Human EST encoded

11	18	8.7	120	22 ABB67378	Drosophila melanog
12	18	8.7	205	22 ABB59297	Drosophila melanog
13	16	7.7	180	19 AAB07874	D. discoideum cycl
14	16	7.7	185	22 AAG65277	Haematopoietic site
15	16	7.7	185	22 AAG65278	Haematopoietic site
16	16	7.7	212	14 AAR32353	Cyclophilin C, Mu
17	15	7.2	58	22 ABB12991	Novel human diagno
18	15	7.2	58	22 ABB29318	Novel human diagno
19	15	7.2	183	21 AAB56701	Human prostate can
20	15	7.2	183	22 ABB66236	Drosophila melanog
21	15	7.2	193	23 ABA42003	Human ovarian anti
22	15	7.2	214	22 ABB23479	Novel human diagno
23	15	7.2	250	22 ABB23480	Novel human diagno
24	13	6.2	125	21 AAG18027	Novel human diagno
25	13	6.2	228	21 AAG18026	Arabidopsis thalia
26	13	6.2	236	21 AAG18025	Arabidopsis thalia
27	13	6.2	737	22 AAG10283	Novel human diagno
28	13	6.2	754	23 AAE24596	Human SR-cyp prote
29	12	5.8	106	22 ABB27275	Novel human diagno
30	12	5.8	114	22 AAB64736	Gene 14 human secr
31	12	5.8	145	12 AAR10763	Porcine peptidyl-P
32	12	5.8	145	16 AAR72917	Porcine peptidyl P
33	12	5.8	145	16 AAR72961	Porcine peptidyl P
34	12	5.8	152	21 AAG08983	Arabidopsis thalia
35	12	5.8	162	21 AAG44157	Arabidopsis thalia
36	12	5.8	163	12 AAR13726	Bovine cyclophilin
37	12	5.8	163	12 AAG65276	Haematopoietic site
38	12	5.8	164	10 AAP90431	Cyclophilin, Homo
39	12	5.8	164	22 AAG65275	Haematopoietic site
40	12	5.8	165	19 AAG56028	Calcineurin protei
41	12	5.8	165	21 AAG03831	Human secreted pro
42	12	5.8	165	22 AAG01195	Human cyclophilin
43	12	5.8	169	22 ABA42929	Human ovarian anti
44	12	5.8	176	21 AAG44156	Arabidopsis thalia
45	12	5.8	184	23 ABA41129	Human ovarian anti

ALIGNMENTS

RESULT 1
ID AAB73301 standard; protein: 216 AA.
XX AAB73301;
AC AAB73301;
XX
XX
DT 22-MAY-2001 (first entry)
XX
DE Human cyclophilin B (Cyph).
XX
KW Human cyclophilin B; Cyph; prolactin-binding; growth hormone-binding;
KW somatotrophic function modulator; immunosuppression; short stature;
KW muscle wasting; osteoporosis; HIV infection; breast cancer;
KW prostate cancer; gigantism; acromegaly; hyperprolactinaemia.
XX
OS Homo sapiens.
XX
XX
XX WO200113113-A1.
XX
XX
XX 22-FEB-2001.
XX
XX 10-AUG-2000; 2000WO-US21789.
XX
XX 19-AUG-1999; 99US-0149752.
XX
XX (UYPE-) UNIV PENNSYLVANIA.
XX
XX Clevenger CV, Ryczyn MA;
XX
XX WPI; 2001-211249/21.
XX
XX Novel composition for modulating somatotrophic function, comprises
PT cyclophilin B, its mutant or an inhibitor of interaction of cyclophilin

PT B with somatotactogenic hormone -
XX
PS Claim 1; Page 17-18; 21pp; English.
XX
CC The invention relates to a composition for modulating somatotactogenic
CC function, comprising cyclophilin B (Cyb), a mutant of cyclophilin B
CC (particularly a Cyb mutant in which residues 2-12 of the mature protein
CC are absent) or an inhibitor of the interaction of cyclophilin B with a
CC somatotactogenic hormone (e.g., prolactin, growth hormone). The invention
CC also relates to a method of identifying inhibitors of somatotactogenic
CC functions using Cyb and a somatotactogenic hormone, and a method for
CC diagnosing diseases associated with abnormal somatotactogenic functions
CC by assessing Cyb levels in a sample from a patient. Cyclophilin B is
CC useful for augmenting somatotactogenic function in the animal, and
CC cyclophilin B mutant or a composition comprising an inhibitor of the
CC interaction of cyclophilin B with a somatotactogenic hormone, is useful
CC for inhibiting somatotactogenic function in the animal. A composition
CC comprising cyclophilin B is useful in the treatment of immunosuppression,
CC in the treatment of short stature, muscle wasting and osteoporosis. A
CC composition comprising cyclophilin B mutant or a composition comprising
CC an inhibitor of the interaction of cyclophilin B with a somatotactogenic
CC hormone, is useful for treating HIV infection, breast and prostate
CC cancer, gigantism/acromegaly, and hyperprolactinaemia. The present
CC sequence represents human cyclophilin B.
XX
SQ Sequence 216 AA:
Query Match 100.0%; Score 208; DB 22; Length 216;
Best Local Similarity 100.0%; Pred. No. 4,9e-194; Mismatches 0; Gaps 0;
Matches 208; Conservative 0; Indels 0;
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QY 1 MKVLLAALIALGVSFFLLPGPSADDEKKKGKRVYKVPDLRIIGDEDVGRVIFGLFGKT 60
DB 9 MKVLLAALIALGVSFFLLPGPSADDEKKKGKRVYKVPDLRIIGDEDVGRVIFGLFGKT 68
QY 61 VPKTVDFVALATGEGFGYKNSKFRHYIKDFMIOGGFTRGDGTGSKSTYGERFPDENF 120
DB 69 VPKTVDFVALATGEGFGYKNSKFRHYIKDFMIOGGFTRGDGTGSKSTYGERFPDENF 128
QY 121 KLKHYPGWVSMANACKDRTNGSOFITTVKTAAMDGKHVVGKVLDEMEVVRKVESTKTD 180
DB 129 KLKHYPGWVSMANACKDRTNGSOFITTVKTAAMDGKHVVGKVLDEMEVVRKVESTKTD 188
QY 181 SRDKPLKDVIIADCGKIEVEKFPALAKE 208
DB 189 SRDKPLKDVIIADCGKIEVEKFPALAKE 216
RESULT 2
AAB43878
ID AAB43878 standard; Protein: 291 AA.
XX
AC AAB43878:
XX
DT 08-FEB-2001 (first entry)
XX
DE Human cancer associated protein sequence SEQ ID NO:1323.
XX
KW Human; cancer associated gene; cancer antigen; detection; cancer;
KW diagnosis; cytostatic; proliferative; vulnerability; immunomodulator;
KW antidiabetic; antistatic; antirheumatic; antiallergic; antiviral;
KW antiinflammatory; antithyroid; antiallergic; antibacterial; cardiant;
KW dermatological; neuroprotective; thrombolytic; coagulant; nootropic;
KW vasotropic; antipsoriatic; antitumorigenic; gene therapy; inflammation;
KW immune disorder; haematopoietic cell disorder; autoimmune disorder;
KW allergic reaction; graft versus host disease; organ rejection;
KW haemostatic; thrombolytic; cardiovascular disorder; infection;
KW neurological disease; drug screening.
XX
OS Homo sapiens.
XX
PN WO200053350-A1.

PD 21-SEP-2000.
XX
XX 08-MAR-2000; 2000MO-US05882.
PF
XX 12-MAR-1999; 99US-0124270.
PR
XX (HUMA-) HUMAN GENOME SCI INC.
PA
XX Rosen CA, Ruben SM:
PI
XX WPI; 2000-587533/55.
XX N-PSDB; AAC78087.
DR
XX
PT Novel isolated nucleic acids comprising sequences encoding peptides
XX useful for treating or diagnosing e.g. cancer -
XX
PS Claim 11; Page 1974-1975; 2352pp; English.
XX
CC AAC77607 to AAC78448 encode the human cancer associated proteins given
CC in AAB43398 to AAB44239. The proteins can have activities based on the
CC tissues and cells the genes are expressed in. Example of activities
CC include: cytostatic; proliferative; vulnerability; immunomodulator;
CC antidiabetic; antistatic; antirheumatic; antiallergic; antibacterial;
CC antiinflammatory; antithyroid; antiallergic; antibacterial; antiviral;
CC dermatological; neuroprotective; cardiant; thrombolytic; coagulant;
CC nootropic; vasotropic; antipsoriatic and antitumorigenic. The
CC polynucleotides and polypeptides can be used for preventing, treating or
CC ameliorating medical conditions and diagnosing pathological conditions.
CC Polynucleotides, polypeptides, antibodies, agonists and antagonists from
CC the present invention may be used to treat immune disorders by activating
CC or inhibiting the proliferation, differentiation or mobilisation of
CC immune cells, to treat disorders of haematopoietic cells, autoimmune
CC disorders, allergic reactions, graft versus host disease and organ
CC rejection, modulate haemostatic or thrombolytic activity, modulate
CC inflammation, cancer, cardiovascular disorders, neurological disease and
CC bacterial or viral infections. The peptides, nucleotides, antibodies and
CC agonists and antagonists may be also be used in drug screens. AAC78449 to
CC AAC78457 and AAB4240 represent sequences used in the exemplification of
CC the present invention.
XX
SQ Sequence 291 AA:
Query Match 100.0%; Score 208; DB 21; Length 291;
Best Local Similarity 100.0%; Pred. No. 6,4e-194; Mismatches 0; Gaps 0;
Matches 208; Conservative 0; Indels 0;
XX
QY 1 MKVLLAALIALGVSFFLLPGPSADDEKKKGKRVYKVPDLRIIGDEDVGRVIFGLFGKT 60
DB 84 MKVLLAALIALGVSFFLLPGPSADDEKKKGKRVYKVPDLRIIGDEDVGRVIFGLFGKT 143
QY 61 VPKTVDFVALATGEGFGYKNSKFRHYIKDFMIOGGFTRGDGTGSKSTYGERFPDENF 120
DB 144 VPKTVDFVALATGEGFGYKNSKFRHYIKDFMIOGGFTRGDGTGSKSTYGERFPDENF 203
QY 121 KLKHYPGWVSMANACKDRTNGSOFITTVKTAAMDGKHVVGKVLDEMEVVRKVESTKTD 180
DB 204 KLKHYPGWVSMANACKDRTNGSOFITTVKTAAMDGKHVVGKVLDEMEVVRKVESTKTD 263
QY 181 SRDKPLKDVIIADCGKIEVEKFPALAKE 208
DB 264 SRDKPLKDVIIADCGKIEVEKFPALAKE 291
RESULT 3
AAB41842
ID AAB41842 standard; Protein: 291 AA.
XX
AC AAB41842:
XX
DT 22-AUG-2002 (first entry)
XX
DE Human ovarian antigen HTFML39, SEQ ID NO:2974.
XX

XX	Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour;
XX	ovarian cancer; breast cancer; tumour; reproductive system disorder;
KM	infertility; pregnancy disorder; anovulation; polycystic ovary syndrome;
KM	PCOS; ovarian cyst; dysmenorrhoea; endocrine disorder; infection;
KM	inflammatory condition; immune disorder; blood disorder;
KM	cardiovascular disorder; respiratory disorder; neurological disorder;
KM	gastrointestinal disorder; urinary system disorder; drug screening;
KM	gene therapy; chromosome mapping; forensic analysis;
KM	antibody preparation; cytostatic; immunomodulatory; neuroprotective;
KM	antiinflammatory; gynaecological; reproductive.
OS	Homo sapiens.
XX	
PN	MO200200677-Al.
XX	
PD	03-JAN-2002.
XX	
XX	07-JUN-2001; 2001WO-US18569.
XX	
XX	07-JUN-2000; 2000US-209467P.
XX	
PA	(HUMA-) HUMAN GENOME SCI INC.
XX	
PI	Birse CE, Rosen CA;
XX	
XX	WPI; 2002-147878/19.
DR	N-PSDB: ABO54919.
XX	
PT	Isolated nucleic acid molecules encoding novel ovarian polypeptides,
PT	useful in the prevention, treatment and diagnosis of cancer (e.g.
PT	ovarian cancer), immune disorders, cardiovascular disorders and
XX	neurological diseases -
XX	
SS	Claim 11; SEQ ID No 2974; 2922pp; English.

Db	84	MKVLLAALLAGSVPFLLLPBSAIDEKKKPKVTVKVFYDLRIGDEVDGRVIFGLHKT	143
OY	61	VPTVDNFVALATGEGKGFGYKNSKFHRYIKDFMIOGGDTLRGDGTGGSIYGERPPDNE	120
Db	144	VPTVDNFVALATGEGKGFGYKNSKFHRYIKDFMIOGGDTLRGDGTGGSIYGERPPDNE	203
OY	121	KLKHFGPGVSNANAGKDTNCSOFFITTVKTAWLDEKHHVFVKVLEGEVRYRVKVESTKTD	180
Db	204	KLKHFGPGVSNANAGKDTNCSOFFITTVKTAWLDEKHHVFVKVLEGEVRYRVKVESTKTD	263
OY	181	SRDKPLKDVILIADCGKIEVEKPFPAIAKE	208
Db	264	SRDKPLKDVILIADCGKIEVEKPFPAIAKE	291

RESULT	4
AA	AA073302
ID	AA073302 standard; protein; 211 AA.
XX	
AC	AA073302;
XX	
DT	22-MAY-2001 (first entry)
XX	
DE	Human cyclophilin B (CypB) C-terminal deletion mutant, CypB-ΔIAKE.
XX	
KW	Human cyclophilin B; CypB; prolactin-binding; growth hormone-binding;
KW	somaolactogenic function modulator; immunosuppression; short stature;
KW	muscle wasting; osteoporosis; HIV infection; breast cancer;
KW	prostate cancer; gigantism; acromegaly; hyperprolactinemia;
KW	C-terminal deletion mutant; mteain.

CC Note: The present sequence is not shown in the specification, but
 CC is derived from the wild-type Cypb sequence shown on pages 17-18.

XX Sequence 211 AA:

Query Match 97.6%; Score 203; DB 22; Length 211;

Best Local Similarity 100.0%; Pred. No. 3.5e-189; Mismatches 0; Indels 0; Gaps 0;

Matches 203; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MKVLLAALAIAGSVFLLLPGPSADDEKKKPKVTVKVFYEDLRIGDEVDGVRVIFGLFGKT 60

9 MKVLLAALAIAGSVFLLLPGPSADDEKKKPKVTVKVFYEDLRIGDEVDGVRVIFGLFGKT 68

61 VPKTVNFPVALATGEGFEGKSKSRHVYIKDFMIOGDFTRGDSGTSGKSTYGERPFDENF 120

69 VPKTVNFPVALATGEGFEGKSKSRHVYIKDFMIOGDFTRGDSGTSGKSTYGERPFDENF 128

121 KLKHVYGVWVSNMACKDYNQSFITVTKTAMLGSKHVYGVKYLEMEYVRKVESTKTD 180

129 KLKHVYGVWVSNMACKDYNQSFITVTKTAMLGSKHVYGVKYLEMEYVRKVESTKTD 188

181 SRDPLKDVIIADCKIEVEKPF 203

189 SRDPLKDVIIADCKIEVEKPF 211

RESULT 5

AAG65273 standard; protein; 183 AA.

20-NOV-2001 (first entry)

Haematopoietic stem cell proliferation agent related human protein #1.

Haematopoietic stem cell proliferation agent; cyclophilin;

dyshemopoiesis; cancer; human; mouse.

Homo sapiens.

JF2001163798-A.

19-JUN-2001.

03-DEC-1999; 99JP-0345542.

03-DEC-1999; 99JP-0345542.

(KANF) KANEKA CORP.

WPI: 2001-592517/67.

Proliferation agent for hematopoietic stem cell containing cyclophilin

Claim 2; Page 13-14; 19pp; Japanese.

The present invention provides a proliferation agent for hematopoietic

stem cells, which contains cyclophilin. This may be used in the treatment

of dyshemopoiesis in radiotherapy and chemotherapy of various

hematopoietic organ diseases and cancers. The present sequence is a

human protein described in the exemplification of the invention.

Sequence 183 AA:

Query Match 88.0%; Score 183; DB 22; Length 183;

Best Local Similarity 100.0%; Pred. No. 8.8e-170; Indels 0; Gaps 0;

Matches 183; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

26 DEKKRGRVTVKVFYEDLRIGDEVDGVRVIFGLFGKTVPKTVNFPVALATGEGFEGKSKSF 85

1 DEKKRGRVTVKVFYEDLRIGDEVDGVRVIFGLFGKTVPKTVNFPVALATGEGFEGKSKSF 60

QY 86 HRVYIKDFMIOGDFTRGDSGTSGKSTYGERPFDENFKLKHVYGVWVSNMACKDYNQSF 145

61 HRVYIKDFMIOGDFTRGDSGTSGKSTYGERPFDENFKLKHVYGVWVSNMACKDYNQSF 120

QY 146 ITTVTKTAMLGSKHVYGVKYLEMEYVRKVESTKTDSDKPLKDVIIADCKIEVEKPF 205

121 ITTVTKTAMLGSKHVYGVKYLEMEYVRKVESTKTDSDKPLKDVIIADCKIEVEKPF 180

QY 206 AKE 208

181 AKE 183

RESULT 6

AAG00090 standard; protein; 166 AA.

06-OCT-2000 (first entry)

Human secreted protein, SEQ ID NO: 4171.

Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;

gene therapy; chromosome mapping.

Homo sapiens.

EP1033401-A2.

06-SEP-2000.

21-FEB-2000; 2000EP-0200610.

26-FEB-1999; 99US-0122487.

(GEST) GENSET.

Dumas Milne Edwards J, Duclert A, Giordano J;

WPI: 2000-500381/45.

N-PSDB; AAC00096.

New nucleic acid that is a 5' expressed sequence tag (5' EST) for

obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for

diagnostic, forensic, gene therapy and chromosome mapping procedures

Claim 13; SEQ ID 4171; 71pp + CD-ROM; English.

The present sequence is a polypeptide encoded by one of a large number

of 5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs

were prepared from total human RNAs or polyA+ RNAs derived from 30

different tissues. EST sequences usually correspond mainly to the 3'

untranslated region (UTR) of the mRNA because they are often obtained

from oligo-dT primed cDNA libraries. Such ESTs are not well suited for

isolating cDNA sequences derived from the 5' ends of mRNAs and even in

those cases where longer cDNA sequences have been obtained, the full 5'

UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5'

ends and can therefore be used to obtain full length cDNAs and genomic

DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and

chromosome mapping procedures. They are used to obtain upstream

regulatory sequences and to design expression and secretion vectors.

Sequence 166 AA:

Query Match 65.9%; Score 137; DB 21; Length 166;

Best Local Similarity 100.0%; Pred. No. 4.5e-125; Indels 0; Gaps 0;

Matches 137; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MKVLLAALAIAGSVFLLLPGPSADDEKKKPKVTVKVFYEDLRIGDEVDGVRVIFGLFGKT 60

9 MKVLLAALAIAGSVFLLLPGPSADDEKKKPKVTVKVFYEDLRIGDEVDGVRVIFGLFGKT 68

OY 61 VKPTVDNFVALATGEGGFGYKNSKFHRVTKDFMIOGGDFTRGDTGSGKSIVGERPPDENF 120
 DB 69 VPKPTVDNFVALATGEGGFGYKNSKFHRVTKDFMIOGGDFTRGDTGSGKSIVGERPPDENF 128
 OY 121 KTKHKGPGWSMANAGK 137
 DB 129 KTKHKGPGWSMANAGK 145

RESULT 7

AA065274 standard; protein; 183 AA.

AC AAG5274;
 DT 20-NOV-2001 (first entry)
 DE Haematopoietic stem cell proliferation agent related murine protein #1.
 XX Haematopoietic stem cell proliferation agent; cyclophilin;
 KM dyshaemopoiesis; cancer; human; mouse.
 XX Mus sp.
 OS JP2001163798-A.
 PN 19-JUN-2001.
 PD 03-DEC-1999; 99JP-0345542.
 PF 03-DEC-1999; 99JP-0345542.
 PR 03-DEC-1999; 99JP-0345542.
 PA (KANE) KANEKA CORP.
 DR WPI; 2001-592517/67.
 XX Proliferation agent for hematopoietic stem cell containing cyclophilin

PT Claim 3; Page 14; 19pp; Japanese.
 PS The present invention provides a proliferation agent for haematopoietic
 CC stem cells, which contains cyclophilin. This may be used in the treatment
 CC of dyshaemopoiesis in radiotherapy and chemotherapy of various
 CC haematopoietic organ diseases and cancers. The present sequence is a
 CC murine protein described in the exemplification of the invention.
 XX Sequence 183 AA;
 SQ

Query Match 47.1%; Score 98; DB 22; Length 183;
 Best Local Similarity 100.0%; Pred. No. 4.2e-87;
 Matches 98; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 54 FGLFEKTYPKPTVDNFVALATGEGGFGYKNSKFHRVTKDFMIOGGDFTRGDTGSGKSIVGE 113
 DB 29 FGLFEKTYPKPTVDNFVALATGEGGFGYKNSKFHRVTKDFMIOGGDFTRGDTGSGKSIVGE 88
 OY 114 RPPDENFKLKHGPGWSMANAGKDTNGSQFFITTYKT 151
 DB 89 RPPDENFKLKHGPGWSMANAGKDTNGSQFFITTYKT 126

RESULT 8

AA099181 standard; Protein; 64 AA.

AC AA099181;
 DT 24-SEP-2002 (first entry)
 DE Partial human perturbation F802.
 XX

KM Retinoid acid pathway; RA; retinoid; lung cancer;
 KM Kaposi's sarcoma; breast cancer; pancreatic cancer; neuroblastoma;
 KM renal cancer; ovarian cancer; dermatitis; hyperkeratosis; eczema;
 KM Darier's disease; Reiter's disease; psoriasis; gene therapy; F797;
 KM acute promyelocytic leukemia; APL; Perturbagen R3; F802; F820;
 KM yeast two-hybrid assay; PRT1; kinesin light chain-related protein;
 KM human.

OS Homo sapiens.
 PN WO200240719-A2.
 PD 23-MAY-2002.
 PF 17-NOV-2001; 2001WO-US44039.
 PR 17-NOV-2000; 2000US-249468P.
 PA (DELTA-) DELTAGEN PROTEOMICS INC.
 PI Kamb CA, Richards BT, Karpilow J;
 DR WPI; 2002-519386/55.
 DR N-PSDB; ABR87379.

PT Polypeptide with retinoid acid pathway activity, especially of
 PT perturbagens R3, F802 and F820 for identifying a cellular target which
 PT interacts with the polypeptide and for therapeutic purposes
 XX Claim 1; Fig 13a; 131pp; English.
 PS The invention relates to an isolated polypeptide (I) with retinoid acid
 CC (RA) pathway activity, comprising a polypeptide sequence of Perturbagen
 CC (phenotypic probe) R3, Perturbagen F802, Perturbagen F820, their
 CC biologically active modifications, or biologically active fragments.
 CC Also included are the polynucleotides encoding the perturbagens, a
 CC vector comprising the polynucleotide, preparing an RA pathway related
 CC polypeptide, a composition comprising the polypeptide, an antibody to the
 CC polypeptide, screening (M) putative RA-related therapeutics, by exposing
 CC the RA pathway polypeptide, to a number of agents, and recovering a
 CC subpopulation of disrupting agents which competitively displace the
 CC polypeptide from the target, where the disrupting agents are putative RA-
 CC related therapeutics. Also include are an isolated RA pathway polypeptide
 CC comprising PRT1 (a kinesin light chain-related protein) polypeptide
 CC and its encoding polynucleotide, a gene therapy vector comprising the RA
 CC pathway protein polypeptide or encoding or PRT1 and a host cell
 CC comprising the gene therapy vector. The RA pathway polypeptide is useful
 CC for identifying a cellular target that interacts with RA pathway-related
 CC polypeptide, by exposing the polypeptide in vitro to putative target
 CC molecules and identifying a polypeptide/target interaction pair, by
 CC detecting reporter expression, where the reporter expression is
 CC operatively linked to the formation of the interaction pair. (M) is a
 CC yeast two-hybrid assay. The polypeptide is also useful for treating
 CC an RA pathway-related condition e.g. lung cancer, Kaposi's sarcoma,
 CC breast cancer, pancreatic cancer, neuroblastoma, renal cancer,
 CC ovarian cancer, dermatitis, hyperkeratosis, eczema, Darier's disease,
 CC Reiter's disease, psoriasis, acute promyelocytic Leukemia (APL).
 CC The present sequence is a partial human perturbation F802.

SO Sequence 64 AA;

Query Match 30.8%; Score 64; DB 23; Length 64;
 Best Local Similarity 100.0%; Pred. No. 1.9e-54;
 Matches 64; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 61 VKPTVDNFVALATGEGGFGYKNSKFHRVTKDFMIOGGDFTRGDTGSGKSIVGERPPDENF 120
 DB 1 VPKPTVDNFVALATGEGGFGYKNSKFHRVTKDFMIOGGDFTRGDTGSGKSIVGERPPDENF 60
 OY 121 KTKH 124
 DB 61 KTKH 64

```

RESULT 9
AA92048
ID AAY92048 standard: Protein; 212 AA.
XX
XX
AC AAY92048;
XX
XX
DT 01-AUG-2000 (first entry)
XX
XX
DE A. niger peptidyl-prolyl cis-trans isomerase (CYPB).
XX
XX
KW Cyclophilin-like peptidyl prolyl cis-trans isomerase; CYPB;
KW food processing; Endoplasmic retention signal; cis-trans isomerization;
KW protein secretion; toxin; ADP-glucose pyrophosphorylase; glucanase;
KW beta-1,4-endoglucanase.
XX
XX
OS Aspergillus niger.
XX
XX
FH Key Location/Qualifiers
FT Peptide 1..23
FT /label= signal_peptide
FT Protein 24..212
FT /label= mature_protein
XX
XX
PN WO200018934-A1.
XX
XX
PD 06-APR-2000.
XX
XX
PF 30-SEP-1999; 99MO-IB01669.
XX
XX
PR 30-SEP-1998; 98GB-0021198.
XX
XX
PA (DANI-) DANISCO AS.
XX
XX
PI Derkx PMF, Madrid SM;
XX
XX
DR WPI: 2000-293167/25.
DR N-PSDB: AAA08772.
XX
XX
PT New peptidyl prolyl cis-trans isomerase, designated CYPB, from
PT Aspergillus niger, useful in methods for increasing the yield of
PT secreted polypeptides, such as enzymes used in food processing, from
PT cells
XX
XX
PS Claim 13; Page 47-48; 52pp; English.
XX
XX
CC This sequence shows Aspergillus niger cyclophilin-like peptidyl prolyl
CC cis-trans isomerase (CYPB). CYPB is capable of catalyzing the cis-trans
CC isomerization of a peptide bond on the N-terminal side of proline
CC residues in polypeptides. CYPB are useful in methods for increasing the
CC yield of secreted polypeptides from cells. The secreted polypeptides may
CC be enzymes (such as chymosin, thrombin or alpha-galactosidase) that can
CC be used in food processing, a pest toxin, adenosine diphosphate
CC (ADP)-glucose pyrophosphorylase, a glucanase or beta-1,4-endoglucanase.
XX
XX
SQ Sequence 212 AA:
XX
XX
Query Match 13.9%; Score 29; DB 21; Length 212;
Best Local Similarity 100.0%; Pred. No. 6,1e-20;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX
QY 85 FHRVYKDFMIQGGDFTRGDGCKSITGE 113
XXXXXXXXXXXXXXXXXXXXXXXXXXXX
DB 84 FHRVYKDFMIQGGDFTRGDGCKSITGE 112
XXXXXXXXXXXXXXXXXXXXXXXXXXXX

```

```

RESULT 10
AAM24287
ID AAM24287 standard: Protein; 83 AA.
XX
XX
AC AAM24287;
XX
XX

```

```

DT 12-OCT-2001 (first entry)
XX
XX
DE Human EST encoded protein SEQ ID NO: 1812.
XX
XX
KW Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse;
KW tomato; monkey; dog; sea urchin; expressed sequence tag; EST;
KW diagnostics; forensic test; gene mapping; genetic disorder;
KW biodiversity; gene therapy; nutrition.
XX
XX
OS Homo sapiens.
XX
XX
PN WO200154477-A2.
XX
XX
PD 02-AUG-2001.
XX
XX
PF 25-JAN-2001; 2001MO-US02687.
XX
XX
PR 25-JAN-2000; 2000US-0491404.
PR 17-JUL-2000; 2000US-0617746.
PR 03-AUG-2000; 2000US-0631451.
PR 15-SEP-2000; 2000US-0663870.
XX
XX
PA (HYSE-) HYSEQ INC.
XX
XX
PI Tang YT, Liu C, Zhou P, Qian XB, Wang Z, Chen R, Asundi V;
PI Cao Y, Drmanac RA, Zhang J, Weirman T;
XX
XX
DR WPI: 2001-476164/51.
DR N-PSDB: AAH98946.
XX
XX
PT Isolated polypeptide for treatment of diseases, diagnostics, raising
PT antibodies and research use -
XX
XX
PS Claim 20; Page 1183-1184; 1275pp; English.
XX
XX
CC The present invention provides the protein and coding sequences of novel
CC proteins from a variety of organisms, including human, dog, cat, horse,
CC cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea
CC urchin and tomato. These were derived from expressed sequence tags (ESTs)
CC from the organism of interest. They can be used in diagnostics,
CC forensics, gene mapping, identification of mutations, to assess
CC biodiversity and for nutritional purposes. The present sequence is a
CC protein of the invention.
XX
XX
SQ Sequence 83 AA:
XX
XX
Query Match 10.6%; Score 22; DB 22; Length 83;
Best Local Similarity 100.0%; Pred. No. 1.7e-13;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX
QY 28 KKKGPKYTVKVVYDLRIGEDV 49
XXXXXXXXXXXXXXXXXXXXXXXXXXXX
DB 28 KKKGPKYTVKVVYDLRIGEDV 49
XXXXXXXXXXXXXXXXXXXXXXXXXXXX

```

```

RESULT 11
ABB67378
ID ABB67378 standard: Protein; 120 AA.
XX
XX
AC ABB67378;
XX
XX
DT 26-MAR-2002 (first entry)
XX
XX
DE Drosophila melanogaster polypeptide SEQ ID NO 28926.
XX
XX
KW Drosophila; developmental biology; cell signalling; insecticide;
KW pharmaceutical.
XX
XX
OS Drosophila melanogaster.
XX
XX
PN WO200171042-A2.
XX
XX
PD 27-SEP-2001.

```


XX 23-MAR-2001; 2001WO-US09231.
 PF 23-MAR-2000; 2000US-191637P.
 PR 11-JUL-2000; 2000US-0614150.
 XX
 PA (PEKE) PE CORP NY.
 XX
 PI Venter JC, Adams M, Li PWD, Myers EW;
 DR N-PSDB; ABL11481.
 XX
 PT New isolated nucleic acid detection reagent for detecting 1000 or more
 PT genes from Drosophila and for elucidating cell signalling and cell-cell
 PT interactions -
 XX
 PS Disclosure; SEQ ID NO 28926; 21pp + Sequence Listing; English.
 XX
 CC The invention relates to an isolated nucleic acid detection reagent
 CC capable of detecting 1000 or more genes from Drosophila. The invention is
 CC useful in developmental biology and in elucidating cell signalling and
 CC cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
 CC sequences (ABL01840-ABL16175) and the encoded proteins
 CC (ABB57737-ABB72072).
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 CC
 CC Sequence 120 AA;
 XX
 SO
 Query Match 8.7%; Score 18; DB 22; Length 120;
 Best Local Similarity 100.0%; Pred. No. 1.9e-09;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 131 SMANAGKDTNGSOFFIT 148
 DB 39 SMANAGKDTNGSOFFIT 56
 XX
 RESULT 12
 ABB59297
 ID ABB59297 standard; Protein; 205 AA.
 XX
 AC ABB59297;
 XX
 DT 26-MAR-2002 (first entry)
 XX
 DE Drosophila melanogaster polypeptide SEQ ID NO 4683.
 XX
 KW Drosophila: developmental biology; cell signalling; insecticide;
 KW pharmaceutical.
 XX
 OS Drosophila melanogaster.
 XX
 MO200171042-A2.
 XX
 PD 27-SEP-2001.
 XX
 PF 23-MAR-2001; 2001WO-US09231.
 XX
 PR 23-MAR-2000; 2000US-191637P.
 PR 11-JUL-2000; 2000US-0614150.
 XX
 PA (PEKE) PE CORP NY.
 XX
 PI Venter JC, Adams M, Li PWD, Myers EW;
 DR N-PSDB; ABL03400.
 XX

PT New isolated nucleic acid detection reagent for detecting 1000 or more
 PT genes from Drosophila and for elucidating cell signalling and cell-cell
 PT interactions -
 XX
 PS Disclosure; SEQ ID NO 4683; 21pp + Sequence Listing; English.
 XX
 CC The invention relates to an isolated nucleic acid detection reagent
 CC capable of detecting 1000 or more genes from Drosophila. The invention is
 CC useful in developmental biology and in elucidating cell signalling and
 CC cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
 CC sequences (ABL01840-ABL16175) and the encoded proteins
 CC (ABB57737-ABB72072).
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 CC
 CC Sequence 205 AA;
 XX
 SO
 Query Match 8.7%; Score 18; DB 22; Length 205;
 Best Local Similarity 100.0%; Pred. No. 3e-09;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 131 SMANAGKDTNGSOFFIT 148
 DB 124 SMANAGKDTNGSOFFIT 141
 XX
 RESULT 13
 AAW80784
 ID AAW80784 standard; Protein; 180 AA.
 XX
 AC AAW80784;
 XX
 DT 07-DEC-1998 (first entry)
 XX
 DE D. discoideum cyclophilin (DdcYP2).
 XX
 KW Dictyostelium; Dp1; discoidin II; human Dp1; hdp1; cyclophilin; DdcYP2;
 KW bisphosphonate binding protein; calcium metabolism; cyclosporine;
 KW osteoporosis; hypercalcaemia; bone metabolism; bone metastases.
 XX
 OS Dictyostelium discoideum.
 XX
 MO9836064-A1.
 XX
 PD 20-AUG-1998.
 XX
 PF 13-FEB-1998; 98WO-US02709.
 XX
 PR 14-FEB-1997; 97US-0039738.
 XX
 PA (PROC) PROCTER & GAMBLE CO.
 PA (UYSH-) UNIV SHEFFIELD MED SCHOOL.
 XX
 PI Cook JS, Ebelino FH, Ibbotson KJ, Ji X, Rogers MJ;
 PI Russell RGCR, Watts DJ, Xiong XJ;
 DR WPI: 1998-506311/43.
 DR N-PSDB; AAV56008.
 XX
 PT Bisphosphonate binding protein - used to treat calcium metabolism
 PT disorders, including bone metabolism, hypercalcaemia, bone
 PT metastases, and osteoporosis
 XX
 PS Claim 5; Fig 21; 98pp; English.
 XX
 CC This represents the amino acid sequence of cyclophilin (DdcYP2) from the
 CC Dictyostelium discoideum Ax-2. The invention provides sequences encoding
 CC Dictyostelium Dp1, human Dp1 (hdp1) and Dictyostelium cyclophilin
 CC (DdcYP2) which are bisphosphonate binding proteins. The invention also
 CC provides methods for purifying and producing such bisphosphonate binding

CC proteins. The bisphosphonate binding protein, or an antibody which binds
 CC to the binding protein can be used in the diagnosis of calcium metabolism
 CC disorders. They can also be used to treat calcium metabolism disorders,
 CC where the treatment is for the regulation of bone metabolism,
 CC hypercalcaemia, bone metastases, and osteoporosis, especially by
 CC regulation of bone metabolism via interaction with cyclosporine.
 CC
 CC

SQ Sequence 180 AA:

Query Match 7.7%; Score 16; DB 19; Length 180;
 Best Local Similarity 100.0%; Pred. No. 2.3e-07;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 92 FMIQGDPTRGDGTGG 107
 |||||
 DB 76 FMIQGDPTRGDGTGG 91

RESULT 14

AAG65277 standard; protein; 185 AA.

AC AAG65277;

DT 20-NOV-2001 (first entry)

XX Haematopoietic stem cell proliferation agent related human protein #3.

XX Haematopoietic stem cell proliferation agent; cyclophilin;

KW dyshaemopoiesis; cancer; human; mouse.

XX Homo sapiens.

PN JP2001163798-A.

PD 19-JUN-2001.

PP 03-DEC-1999; 99JP-0345542.

PR 03-DEC-1999; 99JP-0345542.

PA (KANF) KANEKA CORP.

WPI; 2001-592517/67.

PT Proliferation agent for hematopoietic stem cell containing cyclophilin

PS Disclosure; Page 16-17; 19pp; Japanese.

CC The present invention provides a proliferation agent for haematopoietic
 CC stem cells, which contains cyclophilin. This may be used in the treatment
 CC of dyshaemopoiesis in radiotherapy and chemotherapy of various
 CC haematopoietic organ diseases and cancers. The present sequence is a
 CC human protein described in the exemplification of the invention.
 CC

SQ Sequence 185 AA:

Query Match 7.7%; Score 16; DB 22; Length 185;
 Best Local Similarity 100.0%; Pred. No. 2.4e-07;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 83 SKFRVTKDFMIQGD 98
 |||||
 DB 58 SKFRVTKDFMIQGD 73

RESULT 15

AAG65278 standard; protein; 185 AA.

AC AAG65278;

XX

DT 20-NOV-2001 (first entry)

XX Haematopoietic stem cell proliferation agent related murine protein #3.

XX Haematopoietic stem cell proliferation agent; cyclophilin;

KW dyshaemopoiesis; cancer; human; mouse.

XX Mus sp.

PN JP2001163798-A.

PD 19-JUN-2001.

PP 03-DEC-1999; 99JP-0345542.

PR 03-DEC-1999; 99JP-0345542.

PA (KANF) KANEKA CORP.

WPI; 2001-592517/67.

PT Proliferation agent for hematopoietic stem cell containing cyclophilin

PS Disclosure; Page 17; 19pp; Japanese.

CC The present invention provides a proliferation agent for haematopoietic
 CC stem cells, which contains cyclophilin. This may be used in the treatment
 CC of dyshaemopoiesis in radiotherapy and chemotherapy of various
 CC haematopoietic organ diseases and cancers. The present sequence is a
 CC murine protein described in the exemplification of the invention.
 CC

SQ Sequence 185 AA:

Query Match 7.7%; Score 16; DB 22; Length 185;
 Best Local Similarity 100.0%; Pred. No. 2.4e-07;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 85 FHRVTKDFMIQGDPT 100
 |||||
 DB 60 FHRVTKDFMIQGDPT 75

Search completed: April 10, 2003, 11:54:16
 Job time : 37 secs

GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: April 10, 2003, 11:53:36 ; Search time 15 Seconds
(without alignments)
407,996 Million cell updates/sec

Title: US-09-720-469a-44

Perfect score: 208
Sequence: 1 MKYLAAALLAGSVFLLP.....VIADCKRIEVEKPAFAAKE 208

Scoring table:
Gapop 60.0 , Gapext 60.0

Searched: 262574 seqs, 29422922 residues

Word size : 0

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

Issued_Patents_AA:*
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6: /cgn2_6/prodata/1/laa/Backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	208	100.0	208 1	US-08-142-897-7 Sequence 7, Appl1
2	126	60.6	126 2	US-08-482-728A-10 Sequence 10, Appl1
3	16	7.7	126 2	US-08-482-728A-11 Sequence 11, Appl1
4	16	7.7	212 1	US-08-142-897-5 Sequence 5, Appl1
5	13	6.2	205 1	US-08-142-897-6 Sequence 6, Appl1
6	12	5.8	127 2	US-08-482-728A-9 Sequence 9, Appl1
7	12	5.8	163 1	US-08-142-897-8 Sequence 8, Appl1
8	12	5.8	164 1	US-08-145-995A-9 Sequence 9, Appl1
9	12	5.8	164 2	US-08-451-747-9 Sequence 9, Appl1
10	12	5.8	164 3	US-09-134-852-9 Sequence 9, Appl1
11	12	5.8	165 1	US-08-145-995A-8 Sequence 8, Appl1
12	12	5.8	165 2	US-08-451-747-8 Sequence 8, Appl1
13	12	5.8	165 3	US-09-134-852-8 Sequence 8, Appl1
14	11	5.3	126 2	US-08-482-728A-15 Sequence 15, Appl1
15	11	5.3	134 2	US-08-482-728A-13 Sequence 13, Appl1
16	11	5.3	148 1	US-08-145-995A-6 Sequence 6, Appl1
17	11	5.3	148 2	US-08-451-747-6 Sequence 6, Appl1
18	11	5.3	148 3	US-09-134-852-6 Sequence 6, Appl1
19	11	5.3	162 1	US-08-142-897-9 Sequence 9, Appl1
20	11	5.3	162 2	US-08-145-995A-14 Sequence 14, Appl1
21	11	5.3	162 3	US-08-451-747-14 Sequence 14, Appl1
22	11	5.3	162 4	US-09-134-852-14 Sequence 14, Appl1
23	11	5.3	168 1	US-08-145-995A-12 Sequence 12, Appl1
24	11	5.3	168 2	US-08-451-747-12 Sequence 12, Appl1
25	11	5.3	168 3	US-09-134-852-12 Sequence 12, Appl1
26	11	5.3	169 1	US-08-145-995A-7 Sequence 7, Appl1
27	11	5.3	169 2	US-08-451-747-7 Sequence 7, Appl1

28	11	5.3	169 3	US-09-134-852-7 Sequence 7, Appl1
29	11	5.3	175 1	US-08-145-995A-5 Sequence 5, Appl1
30	11	5.3	175 2	US-08-451-747-5 Sequence 5, Appl1
31	11	5.3	175 3	US-09-134-852-5 Sequence 5, Appl1
32	11	5.3	273 2	US-08-989-386-8 Sequence 8, Appl1
33	10	4.8	109 1	US-08-145-995A-15 Sequence 15, Appl1
34	10	4.8	109 2	US-08-451-747-15 Sequence 15, Appl1
35	10	4.8	109 3	US-09-134-852-15 Sequence 15, Appl1
36	10	4.8	126 2	US-08-482-728A-12 Sequence 12, Appl1
37	10	4.8	134 2	US-08-482-728A-14 Sequence 14, Appl1
38	10	4.8	161 1	US-08-145-995A-13 Sequence 13, Appl1
39	10	4.8	161 2	US-08-451-747-13 Sequence 13, Appl1
40	10	4.8	161 3	US-09-134-852-13 Sequence 13, Appl1
41	10	4.8	171 4	US-09-028-366-7 Sequence 7, Appl1
42	10	4.8	176 1	US-08-145-995A-3 Sequence 3, Appl1
43	10	4.8	176 2	US-08-145-995A-4 Sequence 4, Appl1
44	10	4.8	176 3	US-08-451-747-3 Sequence 3, Appl1
45	10	4.8	176 4	US-08-451-747-4 Sequence 4, Appl1

ALIGNMENTS

RESULT 1
US-08-142-897-7
Sequence 7, Application US/08142897
Patent No. 5447852
GENERAL INFORMATION:
APPLICANT: Friedman, Jeffrey S.
APPLICANT: Weisman, Irving L.
TITLE OF INVENTION: No. 5447852el Cyclophilins, Associating Proteins
TITLE OF INVENTION: and Uses
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Tracy J. Dunn
STREET: One Market Plaza, Stewart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/142,897
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/005,917
FILING DATE: 15-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/740,375
FILING DATE: 05-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: Dunn, Tracy D.
REGISTRATION NUMBER: 34,587
REFERENCE/DOCKET NUMBER: 5490A-92-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 208 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-142-897-7
Query Match 100.0%; Score 208; DB 1; Length 208;
Best Local Similarity 100.0%; Pred. No. 1.4e-188;

Matches 208; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKYLLAALIIASVFFLLLPGRSADEKKKPKTYVYVFDLITGDEGRTVFGFGKT 60
 DB 1 MKYLLAALIIASVFFLLLPGRSADEKKKPKTYVYVFDLITGDEGRTVFGFGKT 60

QY 61 VPKTVDFNVALATGKGGKGYKNSKFRHYIKDFMIOGGDFTIRSDGTGSKSYGERPPDENF 120
 DB 61 VPKTVDFNVALATGKGGKGYKNSKFRHYIKDFMIOGGDFTIRSDGTGSKSYGERPPDENF 120

QY 121 KLHYGPGVSNMANGKDTNKSOFITTYVTAMLDGKHVYGVLEGMVYRVKVESTKTD 180
 DB 121 KLHYGPGVSNMANGKDTNKSOFITTYVTAMLDGKHVYGVLEGMVYRVKVESTKTD 180

QY 181 SRDKPLKDYIADCGKIEVEKFPFAIAKE 208
 DB 181 SRDKPLKDYIADCGKIEVEKFPFAIAKE 208

RESULT 2
 US-08-482-728A-10
 : Sequence 10, Application US/08482728A
 : Patent No. 5968802
 : GENERAL INFORMATION:
 : APPLICANT: Wang, Bruce
 : APPLICANT: Fisher, Joseph
 : APPLICANT: Payan, Donald
 : TITLE OF INVENTION: No. 5968802el Nuclear Cyclophilin
 : NUMBER OF SEQUENCES: 21
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: Flehr, Hombach, Test, Albritton
 : ADDRESSEE: 6 Herbert
 : STREET: Four Embarcadero Center, Suite 3400
 : CITY: San Francisco
 : STATE: California
 : COUNTRY: United States
 : ZIP: 94111-4187
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Floppy disk
 : COMPUTER: IBM PC compatible
 : OPERATING SYSTEM: PC-DOS/MS-DOS
 : SOFTWARE: Patentin Release #1.0, Version #1.30
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/08/482,728A
 : FILING DATE: 07-JUN-1995
 : CLASSIFICATION: 435
 : ATTORNEY/AGENT INFORMATION:
 : NAME: Silva, Robin M.
 : REGISTRATION NUMBER: 38,304
 : REFERENCE/DOCKET NUMBER: A-61230/DJB/RMS
 : TELECOMMUNICATION INFORMATION:
 : TELEPHONE: (415) 781-1989
 : TELEFAX: (415) 398-3249
 : TELEX: 910 277299
 : INFORMATION FOR SEO ID NO: 10:
 : SEQUENCE CHARACTERISTICS:
 : LENGTH: 126 amino acids
 : TYPE: amino acid
 : STRANDEDNESS: unknown
 : TOPOLOGY: unknown
 : MOLECULE TYPE: protein
 : US-08-482-728A-10

Query Match 60.6%; Score 126; DB 2; Length 126;
 Best Local Similarity 100.0%; Pred. No. 1.9e-111;
 Matches 126; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 50 GRVIFGLFGKTVKTVDFNVALATGKGGKGYKNSKFRHYIKDFMIOGGDFTIRSDGTGSKS 109
 DB 1 GRVIFGLFGKTVKTVDFNVALATGKGGKGYKNSKFRHYIKDFMIOGGDFTIRSDGTGSKS 60

QY 110 IYGERPFDENFKLHYGPGVSNMANGKDTNKSOFITTYVTAMLDGKHVYGVLEGMV 169

DB 61 IYGERPFDENFKLHYGPGVSNMANGKDTNKSOFITTYVTAMLDGKHVYGVLEGMV 120

QY 170 VYRKVE 175
 DB 121 VYRKVE 126

RESULT 3
 US-08-482-728A-11
 : Sequence 11, Application US/08482728A
 : Patent No. 5968802
 : GENERAL INFORMATION:
 : APPLICANT: Wang, Bruce
 : APPLICANT: Fisher, Joseph
 : APPLICANT: Payan, Donald
 : TITLE OF INVENTION: No. 5968802el Nuclear Cyclophilin
 : NUMBER OF SEQUENCES: 21
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: Flehr, Hombach, Test, Albritton
 : ADDRESSEE: 6 Herbert
 : STREET: Four Embarcadero Center, Suite 3400
 : CITY: San Francisco
 : STATE: California
 : COUNTRY: United States
 : ZIP: 94111-4187
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Floppy disk
 : COMPUTER: IBM PC compatible
 : OPERATING SYSTEM: PC-DOS/MS-DOS
 : SOFTWARE: Patentin Release #1.0, Version #1.30
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/08/482,728A
 : FILING DATE: 07-JUN-1995
 : CLASSIFICATION: 435
 : ATTORNEY/AGENT INFORMATION:
 : NAME: Silva, Robin M.
 : REGISTRATION NUMBER: 38,304
 : REFERENCE/DOCKET NUMBER: A-61230/DJB/RMS
 : TELECOMMUNICATION INFORMATION:
 : TELEPHONE: (415) 781-1989
 : TELEFAX: (415) 398-3249
 : TELEX: 910 277299
 : INFORMATION FOR SEO ID NO: 11:
 : SEQUENCE CHARACTERISTICS:
 : LENGTH: 126 amino acids
 : TYPE: amino acid
 : STRANDEDNESS: unknown
 : TOPOLOGY: unknown
 : MOLECULE TYPE: protein
 : US-08-482-728A-11

Query Match 7.7%; Score 16; DB 2; Length 126;
 Best Local Similarity 100.0%; Pred. No. 1e-07;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 83 SKFRHYIKDFMIOGGD 98
 DB 34 SKFRHYIKDFMIOGGD 49

RESULT 4
 US-08-142-897-5
 : Sequence 5, Application US/08142897
 : Patent No. 5447852
 : GENERAL INFORMATION:
 : APPLICANT: Friedman, Jeffrey S.
 : APPLICANT: Weisman, Irving L.
 : TITLE OF INVENTION: No. 5447852el Cyclophilins, Associating proteins
 : NUMBER OF SEQUENCES: 10
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: Tracy J. Dunn
 : STREET: One Market Plaza, Stewart Tower, Suite 2000

CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/142,897
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/005,917
FILING DATE: 15-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/740,375
FILING DATE: 05-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: Dunn, Tracy D.
REGISTRATION NUMBER: 34,587
REFERENCE/DOCKET NUMBER: 5490A-92-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 212 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-142-897-5

Query Match
Best Local Similarity 7.7%; Score 16; DB 1; Length 212;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 85 FHRVTKDFMIGDFT 100
|||||
Db 87 FHRVTKDFMIGDFT 102

RESULT 5
US-08-142-897-6
Sequence 6, Application US/08142897
Patent No. 5447852
GENERAL INFORMATION:
APPLICANT: Friedman, Jeffrey S.
APPLICANT: Weissman, Irving L.
TITLE OF INVENTION: No 5447852el Cyclophilins, Associating Proteins
TITLE OF INVENTION: and Uses
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Tracy J. Dunn
STREET: One Market Plaza, Stewart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/142,897
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/005,917
FILING DATE: 15-JAN-1993
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/740,375
FILING DATE: 05-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: Dunn, Tracy D.
REGISTRATION NUMBER: 34,587
REFERENCE/DOCKET NUMBER: 5490A-92-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 205 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-142-897-6

Query Match
Best Local Similarity 6.2%; Score 13; DB 1; Length 205;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 136 GDTNQSOFITTT 148
|||||
Db 137 GDTNQSOFITTT 149

RESULT 6
US-08-482-728A-9
Sequence 9, Application US/08482728A
Patent No. 5968802
GENERAL INFORMATION:
APPLICANT: Wang, Bruce
APPLICANT: Fisher, Joseph
APPLICANT: Payan, Donald
TITLE OF INVENTION: No. 5968802el Nuclear Cyclophilin
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Flehr, Hohnbach, Test, Albritton
ADDRESS: 6 Herbert
STREET: Four Embardadero Center, Suite 3400
CITY: San Francisco
STATE: California
COUNTRY: United States
ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,728A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Silva, Robin M.
REGISTRATION NUMBER: 38,304
REFERENCE/DOCKET NUMBER: A-61230/DJB/RMS
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1889
TELEFAX: (415) 398-3249
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 127 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-482-728A-9

Query Match
Best Local Similarity 5.8%; Score 12; DB 2; Length 127;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 153 WLDGKHVFGKV 164
|||||
Db 104 WLDGKHVFGKV 115

RESULT 7

US-08-142-897-8
; Sequence 8, Application US/08142897
; Patent No. 5447852
; GENERAL INFORMATION:
; APPLICANT: Friedman, Jeffrey S.
; TITLE OF INVENTION: No. 5447852el Cyclophilins, Associating Proteins
; TITLE OF INVENTION: And Uses
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Tracy J. Dunn
; STREET: One Market Plaza, Stewart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/142,897
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/005,917
; FILING DATE: 15-JAN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/740,375
; FILING DATE: 05-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Dunn, Tracy D.
; REGISTRATION NUMBER: 34,587
; REFERENCE/DOCKET NUMBER: 5490A-92-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 163 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-142-897-8

Query Match 5.8%; Score 12; DB 1; Length 163;
Best Local Similarity 100.0%; Pred. No. 0.00074;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 153 WLDGKHVFGKV 164
|||||
Db 120 WLDGKHVFGKV 131

RESULT 8

US-08-145-995A-9
; Sequence 9, Application US/08145995A
; Patent No. 5482850
; GENERAL INFORMATION:
; APPLICANT: CARLOW, CLOTILDE K.S.
; APPLICANT: PAGE, ANTONY
; TITLE OF INVENTION: METHOD FOR IDENTIFYING ANTI-PARASITIC
; TITLE OF INVENTION: COMPOUNDS

NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &
ADDRESSEE: CUSHMAN
STREET: 130 WATER STREET
CITY: BOSTON
STATE: MASSACHUSETTS
COUNTRY: USA
ZIP: 02109

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/145,995A
FILING DATE: 29-OCT-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: RESNICK, DAVID S.
REGISTRATION NUMBER: 34235
REFERENCE/DOCKET NUMBER: 43406
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 523-3400
TELEFAX: (617) 523-6440
TELEX: 200291 STRE UR
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 164 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-145-995A-9

Query Match 5.8%; Score 12; DB 1; Length 164;
Best Local Similarity 100.0%; Pred. No. 0.00075;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 153 WLDGKHVFGKV 164
|||||
Db 121 WLDGKHVFGKV 132

RESULT 9
US-08-451-747-9
; Sequence 9, Application US/08451747
; Patent No. 5821107
; GENERAL INFORMATION:
; APPLICANT: CARLOW, CLOTILDE K.S.
; APPLICANT: PAGE, ANTONY
; TITLE OF INVENTION: METHOD FOR IDENTIFYING ANTI-PARASITIC
; TITLE OF INVENTION: COMPOUNDS
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GREGORY D. WILLIAMS; NEW ENGLAND BIOLABS, INC.
; STREET: 32 TOZER ROAD
; CITY: BEVERLY
; STATE: MASSACHUSETTS
; COUNTRY: USA
; ZIP: 01915

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/451,747
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/145,995
FILING DATE: 29-OCT-1993

CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: WILLIAMS, GREGORY D.
REGISTRATION NUMBER: 30901
REFERENCE/DOCKET NUMBER: NEB-046-DIV
TELECOMMUNICATION INFORMATION:
TELEPHONE: (508) 927-5054
TELEFAX: (508) 927-1705
TELEX:
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 164 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-451-747-9

Query Match 5.8%; Score 12; DB 2; Length 164;
Best Local Similarity 100.0%; Pred. No. 0.00075;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 153 WLDGKHVFGKV 164
|||||
Db 121 WLDGKHVFGKV 132

RESULT 10
US-09-134-852-9
Sequence 9, Application US/09134852
Patent No. 6127148
GENERAL INFORMATION:
APPLICANT: CARLOW, CLOTTIDE K.S.
TITLE OF INVENTION: METHOD FOR IDENTIFYING ANTI-PARASITIC
TITLE OF INVENTION: COMPOUNDS
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &
ADDRESS: CUSHMAN
STREET: 130 WATER STREET
CITY: BOSTON
STATE: MASSACHUSETTS
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/134,852
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/145,995
FILING DATE: 29-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: RESNICK, DAVID S.
REGISTRATION NUMBER: 34235
REFERENCE/DOCKET NUMBER: 43406
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 523-3400
TELEFAX: (617) 523-6440
TELEX: 200291 STRE UR
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 164 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-09-134-852-9

Query Match 5.8%; Score 12; DB 3; Length 164;
Best Local Similarity 100.0%; Pred. No. 0.00075;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 153 WLDGKHVFGKV 164
|||||
Db 121 WLDGKHVFGKV 132

RESULT 11
US-08-145-995A-8
Sequence 8, Application US/08145995A
Patent No. 5482850
GENERAL INFORMATION:
APPLICANT: CARLOW, CLOTTIDE K.S.
TITLE OF INVENTION: METHOD FOR IDENTIFYING ANTI-PARASITIC
TITLE OF INVENTION: COMPOUNDS
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &
ADDRESS: CUSHMAN
STREET: 130 WATER STREET
CITY: BOSTON
STATE: MASSACHUSETTS
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/145,995A
FILING DATE: 29-OCT-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: RESNICK, DAVID S.
REGISTRATION NUMBER: 34235
REFERENCE/DOCKET NUMBER: 43406
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 523-3400
TELEFAX: (617) 523-6440
TELEX: 200291 STRE UR
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 165 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-145-995A-8

Query Match 5.8%; Score 12; DB 1; Length 165;
Best Local Similarity 100.0%; Pred. No. 0.00075;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 153 WLDGKHVFGKV 164
|||||
Db 121 WLDGKHVFGKV 132

RESULT 12
US-08-451-747-8
Sequence 8, Application US/08451747
Patent No. 5821107
GENERAL INFORMATION:
APPLICANT: CARLOW, CLOTTIDE K.S.
TITLE OF INVENTION: METHOD FOR IDENTIFYING ANTI-PARASITIC
TITLE OF INVENTION: COMPOUNDS
NUMBER OF SEQUENCES: 21

;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: GREGORY D. WILLIAMS, NEW ENGLAND BIOLABS, INC.
;; STREET: 32 TOZER ROAD
;; CITY: BEVERLY
;; STATE: MASSACHUSETTS
;; COUNTRY: USA
;; ZIP: 01915
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patentin Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/451,747
;; FILING DATE:
;; CLASSIFICATION: 514
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/145,995
;; FILING DATE: 29-OCT-1993
;; CLASSIFICATION: 514
;; ATTORNEY/AGENT INFORMATION:
;; NAME: WILLIAMS, GREGORY D.
;; REGISTRATION NUMBER: 30901
;; REFERENCE/DOCKET NUMBER: NEB-046-DIV
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (508) 927-5054
;; TELEFAX: (508) 927-1705
;; TELEX:
;;
;; INFORMATION FOR SEQ ID NO: 8:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 165 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: unknown
;; TOPOLOGY: unknown
;; MOLECULE TYPE: protein
;; US-08-451-747-8
;
Query Match 5.8%; Score 12; DB 2; Length 165;
Best Local Similarity 100.0%; Pred. No. 0 00075;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 153 WLDGKHVFGKV 164
Db 121 WLDGKHVFGKV 132

;; RESULT 13
;; US-09-134-852-8
;; Sequence 8, Application US/09134852
;; Patent No. 6127148
;;
;; GENERAL INFORMATION:
;; APPLICANT: CARLOW, CLOTTIDE K.S.
;; APPLICANT: PAGE, ANTONY
;; TITLE OF INVENTION: METHOD FOR IDENTIFYING ANTI-PARASITIC
;; TITLE OF INVENTION: COMPOUNDS
;; NUMBER OF SEQUENCES: 21
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: DAVID G. CONLIN, DIKE, BRONSTEIN, ROBERTS &
;; STREET: 130 WATER STREET
;; CITY: BOSTON
;; STATE: MASSACHUSETTS
;; COUNTRY: USA
;; ZIP: 02109
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patentin Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/134,852
;; FILING DATE:
;; CLASSIFICATION:

;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/145,995
;; FILING DATE: 29-OCT-1993
;; ATTORNEY/AGENT INFORMATION:
;; NAME: RESNICK, DAVID S.
;; REGISTRATION NUMBER: 34235
;; REFERENCE/DOCKET NUMBER: 43406
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (617) 523-3400
;; TELEFAX: (617) 523-6440
;; TELEX: 200291 STRE UR
;; INFORMATION FOR SEQ ID NO: 8:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 165 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: unknown
;; TOPOLOGY: unknown
;; MOLECULE TYPE: protein
;; US-09-134-852-8
;
Query Match 5.8%; Score 12; DB 3; Length 165;
Best Local Similarity 100.0%; Pred. No. 0 00075;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 153 WLDGKHVFGKV 164
Db 121 WLDGKHVFGKV 132

;; RESULT 14
;; US-08-482-728A-16
;; Sequence 16, Application US/08482728A
;; Patent No. 5968802
;;
;; GENERAL INFORMATION:
;; APPLICANT: Wang, Bruce
;; APPLICANT: Fisher, Joseph
;; APPLICANT: Payan, Donald
;; TITLE OF INVENTION: No. 5968802el Nuclear Cyclophilin
;; NUMBER OF SEQUENCES: 21
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Flehr, Hohbach, Test, Albritton
;; STREET: Four Embarcadero Center, Suite 3400
;; CITY: San Francisco
;; STATE: California
;; COUNTRY: United States
;; ZIP: 94111-4187
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patentin Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/482,728A
;; FILING DATE: 07-JUN-1995
;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:
;; NAME: SILVA, Robin M.
;; REGISTRATION NUMBER: 38,304
;; REFERENCE/DOCKET NUMBER: A-61230/DJB/RMS
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (415) 781-1989
;; TELEFAX: (415) 398-3249
;; TELEX: 910 277299
;; INFORMATION FOR SEQ ID NO: 16:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 126 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: unknown
;; TOPOLOGY: unknown
;; MOLECULE TYPE: protein
;; US-08-482-728A-16

Query Match 5.3%; Score 11; DB 2; Length 126;
 Best Local Similarity 100.0%; Pred. No. 0.0052;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 139 TNGSQFFITTV 149
 |||||
 DB 90 TNGSQFFITTV 100

RESULT 15

US-08-482-728A-13
 ; Sequence 13, Application US/08482728A
 ; Patent No. 5968802
 ; GENERAL INFORMATION:
 ; APPLICANT: Wang, Bruce
 ; APPLICANT: Fisher, Joseph
 ; APPLICANT: Pavan, Donald
 ; TITLE OF INVENTION: No. 5968802el Nuclear Cyclophilin
 ; NUMBER OF SEQUENCES: 21
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Flehr, Hohbach, Test, Albritton
 ; ADDRESSEE: & Herbert
 ; STREET: Four Embarcadero Center, Suite 3400
 ; CITY: San Francisco
 ; STATE: California
 ; COUNTRY: United States
 ; ZIP: 94111-4187
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/482,728A
 ; FILING DATE: 07-JUN-1995
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Silva, Robin M.
 ; REGISTRATION NUMBER: 38,304
 ; REFERENCE/DOCKET NUMBER: A-61230/DJB/RMS
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (415) 781-1989
 ; TELEFAX: (415) 398-3249
 ; TELEX: 910 277299
 ; INFORMATION FOR SEQ ID NO: 13:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 134 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: unknown
 ; TOPOLOGY: unknown
 ; MOLECULE TYPE: protein
 ; US-08-482-728A-13

Query Match 5.3%; Score 11; DB 2; Length 134;
 Best Local Similarity 100.0%; Pred. No. 0.0055;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 139 TNGSQFFITTV 149
 |||||
 DB 98 TNGSQFFITTV 108

Search completed: April 10, 2003, 11:56:00
 Job time : 16 secs

Db 181 SRDPLKDVIIADCGKIEVEKFFATAKE 208

RESULT 2

US-09-925-301-1323
Sequence 1323, Application US/09925301
Patent No. US20020052308A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA106
CURRENT APPLICATION NUMBER: US/09/925,301
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05882
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1694
SOFTWARE: Patentln Ver. 2.0
SEQ ID NO 1323
LENGTH: 291
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: (30)
OTHER INFORMATION: xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (57)
OTHER INFORMATION: xaa equals any of the naturally occurring L-amino acids
US-09-925-301-1323

Query Match 100.0%; Score 208; DB 10; Length 291;
Best Local Similarity 100.0%; Pred. No. 1,2e-189;
Matches 208; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKVLLAAALIASVFFLLPGPSADENKKGPVYVYFDLRIGDGVGRVIFGLFGKT 60
DB 84 MKVLLAAALIASVFFLLPGPSADENKKGPVYVYFDLRIGDGVGRVIFGLFGKT 143
QY 61 VPTVTVNFVALATGEGFEGYKNSKFRHYIKDFMIOGDFTRGDTGSGKSYGRPDENP 120
DB 144 VPTVTVNFVALATGEGFEGYKNSKFRHYIKDFMIOGDFTRGDTGSGKSYGRPDENP 203
QY 121 KLRHYPGWVSMANAGKDTNGSOFFITTVKTAMLGDKHVFEGKYLEGMEYVRVVESTKTD 180
DB 204 KLRHYPGWVSMANAGKDTNGSOFFITTVKTAMLGDKHVFEGKYLEGMEYVRVVESTKTD 263
QY 181 SRDPLKDVIIADCGKIEVEKFFATAKE 208
DB 264 SRDPLKDVIIADCGKIEVEKFFATAKE 291

RESULT 3

US-10-043-142-11
Sequence 11, Application US/10043142
Patent No. US20020150969A1
GENERAL INFORMATION:
APPLICANT: DERKX, PATRICK M.F.
APPLICANT: MADRID, SUSAN M.
TITLE OF INVENTION: PEPTIDYL PROLYL CIS-TRANS ISOMERASES
FILE REFERENCE: 078883/0128
CURRENT APPLICATION NUMBER: US/10/043,142
CURRENT FILING DATE: 2002-01-14
PRIOR APPLICATION NUMBER: 09/806,399
PRIOR FILING DATE: 2002-03-30
PRIOR APPLICATION NUMBER: PCT/IB99/01669
PRIOR FILING DATE: 1999-09-30
PRIOR APPLICATION NUMBER: GB 9821198.0
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentln Ver. 2.1

SEQ ID NO 11
LENGTH: 207
TYPE: PRT
ORGANISM: Mus musculus
US-10-043-142-11

Query Match 26.4%; Score 55; DB 12; Length 207;
Best Local Similarity 100.0%; Pred. No. 1,4e-44;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 114 RPPDENFKLKHYPGWVSMANAGKDTNGSOFFITTVKTAMLGDKHVFEGKYLEGM 168
DB 113 RPPDENFKLKHYPGWVSMANAGKDTNGSOFFITTVKTAMLGDKHVFEGKYLEGM 167

RESULT 4

US-10-043-142-10
Sequence 10, Application US/10043142
Patent No. US20020150969A1
GENERAL INFORMATION:
APPLICANT: DERKX, PATRICK M.F.
APPLICANT: MADRID, SUSAN M.
TITLE OF INVENTION: PEPTIDYL PROLYL CIS-TRANS ISOMERASES
FILE REFERENCE: 078883/0128
CURRENT APPLICATION NUMBER: US/10/043,142
CURRENT FILING DATE: 2002-01-14
PRIOR APPLICATION NUMBER: 09/806,399
PRIOR FILING DATE: 2002-03-30
PRIOR APPLICATION NUMBER: PCT/IB99/01669
PRIOR FILING DATE: 1999-09-30
PRIOR APPLICATION NUMBER: GB 9821198.0
PRIOR FILING DATE: 1998-09-30
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentln Ver. 2.1
SEQ ID NO 10
LENGTH: 203
TYPE: PRT
ORGANISM: Ophiomyces sp.
US-10-043-142-10

Query Match 17.8%; Score 37; DB 12; Length 203;
Best Local Similarity 100.0%; Pred. No. 1,7e-27;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 79 GYKNSKFRHYIKDFMIOGDFTRGDTGSGKSYGERF 115
DB 73 GYKNSKFRHYIKDFMIOGDFTRGDTGSGKSYGERF 109

RESULT 5

US-10-043-142-5
Sequence 5, Application US/10043142
Patent No. US20020150969A1
GENERAL INFORMATION:
APPLICANT: DERKX, PATRICK M.F.
APPLICANT: MADRID, SUSAN M.
TITLE OF INVENTION: PEPTIDYL PROLYL CIS-TRANS ISOMERASES
FILE REFERENCE: 078883/0128
CURRENT APPLICATION NUMBER: US/10/043,142
CURRENT FILING DATE: 2002-01-14
PRIOR APPLICATION NUMBER: 09/806,399
PRIOR FILING DATE: 2002-03-30
PRIOR APPLICATION NUMBER: PCT/IB99/01669
PRIOR FILING DATE: 1999-09-30
PRIOR APPLICATION NUMBER: GB 9821198.0
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentln Ver. 2.1
SEQ ID NO 5
LENGTH: 212
TYPE: PRT
ORGANISM: Aspergillus niger
US-10-043-142-5

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Query Match      13.98; Score 29; DB 12; Length 212;
Best Local Similarity 100.0%; Pred. No. 6.8e-20;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      85 FHRVVKDFMIOGDFTRGDDTGKSIYGE 113
      ||||||||||||||||||||||||||||
DB      84 FHRVVKDFMIOGDFTRGDDTGKSIYGE 112

RESULT 6
US-09-925-300-1279
; Sequence 1279, Application US/09925300
; Patent No. US20020151681A1
; GENERAL INFORMATION:
; APPLICANT: Craig Rosen,
; APPLICANT: Steve Ruben
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA101
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05988
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1690
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1279
; LENGTH: 183
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-925-300-1279

Query Match      7.28; Score 15; DB 10; Length 183;
Best Local Similarity 100.0%; Pred. No. 1.1e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      85 FHRVVKDFMIOGDF 99
      ||||||||||||||||
DB      71 FHRVVKDFMIOGDF 85

RESULT 7
US-09-864-761-40591
; Sequence 40591, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aecomica-X-1
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263,6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
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; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 40591
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AP001538.1
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 11
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 3.2
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 2.8
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 3.6
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.5
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.6
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 10
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 16
; OTHER INFORMATION: EST_HUMAN HIT: BF244231.1, EVALUATE 3.00e-56
; OTHER INFORMATION: SWISSPROT HIT: P05092, EVALUATE 2.00e-49
US-09-864-761-40591

Query Match      4.88; Score 10; DB 10; Length 108;
Best Local Similarity 100.0%; Pred. No. 0.039;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      104 GTGGSKIYGE 113
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DB      91 GTGGSKIYGE 100

RESULT 8
US-10-028-072-8
; Sequence 8, Application US/10028072
; Publication No. US20030004311A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerlitsen, Matly E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Watanabe, William
; APPLICANT: Zhang
; TITLE OF INVENTION:
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/028,072
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1 CURRENT FILING DATE: 2001-12-19
2 PRIOR APPLICATION NUMBER: 60/04911
3 PRIOR FILING DATE: 1997-06-18
4 PRIOR APPLICATION NUMBER: 60/056974
5 PRIOR FILING DATE: 1997-08-26
6 PRIOR APPLICATION NUMBER: 60/059113
7 PRIOR FILING DATE: 1997-09-17
8 PRIOR APPLICATION NUMBER: 60/059115
9 PRIOR FILING DATE: 1997-09-17
10 PRIOR APPLICATION NUMBER: 60/059117
11 PRIOR FILING DATE: 1997-09-17
12 PRIOR APPLICATION NUMBER: 60/059122
13 PRIOR FILING DATE: 1997-09-17
14 PRIOR APPLICATION NUMBER: 60/059184
15 PRIOR FILING DATE: 1997-09-17
16 PRIOR APPLICATION NUMBER: 60/059263
17 PRIOR FILING DATE: 1997-09-18
18 PRIOR APPLICATION NUMBER: 60/05352
19 PRIOR FILING DATE: 1997-09-19
20 PRIOR APPLICATION NUMBER: 60/05588
21 PRIOR FILING DATE: 1997-09-19
22 PRIOR APPLICATION NUMBER: 60/059836
23 PRIOR FILING DATE: 1997-09-24
24 PRIOR APPLICATION NUMBER: 60/062250
25 PRIOR FILING DATE: 1997-10-17
26 PRIOR APPLICATION NUMBER: 60/062285
27 PRIOR FILING DATE: 1997-10-17
28 PRIOR APPLICATION NUMBER: 60/062287
29 PRIOR FILING DATE: 1997-10-17
30 PRIOR APPLICATION NUMBER: 60/062814
31 PRIOR FILING DATE: 1997-10-24
32 PRIOR APPLICATION NUMBER: 60/062816
33 PRIOR FILING DATE: 1997-10-24
34 PRIOR APPLICATION NUMBER: 60/063045
35 PRIOR FILING DATE: 1997-10-24
36 PRIOR APPLICATION NUMBER: 60/063082
37 PRIOR FILING DATE: 1997-10-31
38 PRIOR APPLICATION NUMBER: 60/063127
39 PRIOR FILING DATE: 1997-10-24
40 PRIOR APPLICATION NUMBER: 60/063327
41 PRIOR FILING DATE: 1997-10-27
42 PRIOR APPLICATION NUMBER: 60/063329
43 PRIOR FILING DATE: 1997-10-27
44 PRIOR APPLICATION NUMBER: 60/063550
45 PRIOR FILING DATE: 1997-10-28
46 PRIOR APPLICATION NUMBER: 60/063561
47 PRIOR FILING DATE: 1997-10-28
48 PRIOR APPLICATION NUMBER: 60/063704
49 PRIOR FILING DATE: 1997-10-29
50 PRIOR APPLICATION NUMBER: 60/063733
51 PRIOR FILING DATE: 1997-10-29
52 PRIOR APPLICATION NUMBER: 60/063735
53 PRIOR FILING DATE: 1997-10-29
54 PRIOR APPLICATION NUMBER: 60/063738
55 PRIOR FILING DATE: 1997-10-29
56 PRIOR APPLICATION NUMBER: 60/063755
57 PRIOR FILING DATE: 1997-10-17
58 PRIOR APPLICATION NUMBER: 60/064248
59 PRIOR FILING DATE: 1997-11-03
60 PRIOR APPLICATION NUMBER: 60/064809
61 PRIOR FILING DATE: 1997-11-07
62 PRIOR APPLICATION NUMBER: 60/065186
63 PRIOR FILING DATE: 1997-11-12
64 PRIOR APPLICATION NUMBER: 60/065846
65 PRIOR FILING DATE: 1997-11-17
66 PRIOR APPLICATION NUMBER: 60/066364
67 PRIOR FILING DATE: 1997-11-21
68 PRIOR APPLICATION NUMBER: 60/066453
69 PRIOR FILING DATE: 1997-11-24
70 PRIOR APPLICATION NUMBER: 60/066511
71 PRIOR FILING DATE: 1997-11-24
72 PRIOR APPLICATION NUMBER: 60/066770
73 PRIOR FILING DATE: 1997-11-24

74 PRIOR APPLICATION NUMBER: 60/069212
75 PRIOR FILING DATE: 1997-12-11
76 PRIOR APPLICATION NUMBER: 60/069278
77 PRIOR FILING DATE: 1997-12-11
78 PRIOR APPLICATION NUMBER: 60/069334
79 PRIOR FILING DATE: 1997-12-11
80 PRIOR APPLICATION NUMBER: 60/069694
81 PRIOR FILING DATE: 1997-12-16
82 PRIOR APPLICATION NUMBER: 60/072320
83 PRIOR FILING DATE: 1998-01-23
84 PRIOR APPLICATION NUMBER: 60/073612
85 PRIOR FILING DATE: 1998-02-04
86 PRIOR APPLICATION NUMBER: 60/074086
87 PRIOR FILING DATE: 1998-02-09
88 PRIOR APPLICATION NUMBER: 60/074092
89 PRIOR FILING DATE: 1998-02-09
90 PRIOR APPLICATION NUMBER: 60/077791
91 PRIOR FILING DATE: 1998-03-12
92 PRIOR APPLICATION NUMBER: 60/078910
93 PRIOR FILING DATE: 1998-03-20
94 PRIOR APPLICATION NUMBER: 60/079294
95 PRIOR FILING DATE: 1998-03-25
96 PRIOR APPLICATION NUMBER: 60/079663
97 PRIOR FILING DATE: 1998-02-27
98 PRIOR APPLICATION NUMBER: 60/079728
99 PRIOR FILING DATE: 1998-03-27
100 PRIOR APPLICATION NUMBER: 60/080165
101 PRIOR FILING DATE: 1998-03-31
102 PRIOR APPLICATION NUMBER: 60/081203
103 PRIOR FILING DATE: 1998-04-09
104 PRIOR APPLICATION NUMBER: 60/081229
105 PRIOR FILING DATE: 1998-04-09
106 PRIOR APPLICATION NUMBER: 60/081695
107 PRIOR FILING DATE: 1998-04-14
108 PRIOR APPLICATION NUMBER: 60/081817
109 PRIOR FILING DATE: 1998-04-15
110 PRIOR APPLICATION NUMBER: 60/081818
111 PRIOR FILING DATE: 1998-04-15
112 PRIOR APPLICATION NUMBER: 60/082999
113 PRIOR FILING DATE: 1998-04-24
114 PRIOR APPLICATION NUMBER: 60/083322
115 PRIOR FILING DATE: 1998-04-28
116 PRIOR APPLICATION NUMBER: 60/083545
117 PRIOR FILING DATE: 1998-04-29
118 PRIOR APPLICATION NUMBER: 60/084600
119 PRIOR FILING DATE: 1998-05-07
120 PRIOR APPLICATION NUMBER: 60/084627
121 PRIOR FILING DATE: 1998-05-07
122 PRIOR APPLICATION NUMBER: 60/084637
123 PRIOR FILING DATE: 1998-05-07
124 PRIOR APPLICATION NUMBER: 60/085149
125 PRIOR FILING DATE: 1998-05-12
126 PRIOR APPLICATION NUMBER: 60/085323
127 PRIOR FILING DATE: 1998-05-13
128 PRIOR APPLICATION NUMBER: 60/085338
129 PRIOR FILING DATE: 1998-05-13
130 PRIOR APPLICATION NUMBER: 60/085339
131 PRIOR FILING DATE: 1998-05-13
132 PRIOR APPLICATION NUMBER: 60/085579
133 PRIOR FILING DATE: 1998-05-15
134 PRIOR APPLICATION NUMBER: 60/085697
135 PRIOR FILING DATE: 1998-05-15
136 PRIOR APPLICATION NUMBER: 60/085704
137 PRIOR FILING DATE: 1998-05-15
138 PRIOR APPLICATION NUMBER: 60/086414
139 PRIOR FILING DATE: 1998-05-22
140 PRIOR APPLICATION NUMBER: 60/086430
141 PRIOR FILING DATE: 1998-05-22
142 PRIOR APPLICATION NUMBER: 60/087106
143 PRIOR FILING DATE: 1998-05-28
144 PRIOR APPLICATION NUMBER: 60/088026
145 PRIOR FILING DATE: 1998-06-04
146 PRIOR APPLICATION NUMBER: 60/088730

PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088741
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088810
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088858
PRIOR FILING DATE: 19/98-06-11
PRIOR APPLICATION NUMBER: 60/089532
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089599
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089907
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089947
PRIOR FILING DATE: 1998-06-19
PRIOR APPLICATION NUMBER: 60/090349
PRIOR FILING DATE: 1998-06-23
PRIOR APPLICATION NUMBER: 60/090429
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090445
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090538
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090863
PRIOR FILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: 60/091360
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091519
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07

Query Match
Best Local Similarity 4.8%; Score 10; DB 9; Length 166;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 89 IKDFMIOGCD 98
Db 57 IKDFMIOGCD 66

RESULT 9
US-10-121-049-8

Sequence 8, Application US/10121049
Publication No. US2003002239A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: DeForge, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Sherwood, Steven
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3330R1C17
CURRENT FILING DATE: 2002-04-12
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 8
LENGTH: 166
TYPE: PRT

ORGANISM: Homo Sapien
US-10-121-049-8

Query Match
Best Local Similarity 4.8%; Score 10; DB 9; Length 166;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 89 IKDFMIOGCD 98
Db 57 IKDFMIOGCD 66

RESULT 10
US-10-123-904-8

Sequence 8, Application US/10123904
Publication No. US20030022328A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: DeForge, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Sherwood, Steven
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3330R1C54
CURRENT FILING DATE: 2002-04-16
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 8
LENGTH: 166
TYPE: PRT
ORGANISM: Homo Sapien
US-10-123-904-8

Query Match
Best Local Similarity 4.8%; Score 10; DB 9; Length 166;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 89 IKDFMIOGCD 98
Db 57 IKDFMIOGCD 66

RESULT 11
US-10-140-470-8

Sequence 8, Application US/10140470
Publication No. US20030022331A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: DeForge, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Sherwood, Steven
APPLICANT: Smith, Victoria

```

: APPLICANT: Stewart,Timothy A.
: APPLICANT: Tumas,Daniel
: APPLICANT: Watanabe,Colin K
: APPLICANT: Wood,William
: APPLICANT: Zhang,Zemin
: TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
: FILE REFERENCE: P3330R1C160
: CURRENT APPLICATION NUMBER: US/10/140,470
: CURRENT FILING DATE: 2002-05-06
: Prior Application removed - See Palm or File Wrapper
: NUMBER OF SEQ ID NOS: 550
: SEQ ID NO 8
: LENGTH: 166
: TYPE: PRT
: ORGANISM: Homo Sapien
US-10-140-470-8

Query Match
Best Local Similarity 4.8%; Score 10; DB 9; Length 166;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 89 IKDFMIQGD 98
DB 57 IKDFMIQGD 66

RESULT 12
US-10-175-746-8
: Sequence 8, Application US/10175746
: Publication No. US20030027270A1
: GENERAL INFORMATION:
: APPLICANT: Baker,Kevin P.
: APPLICANT: Beresini,Maureen
: APPLICANT: Deforge,Laura
: APPLICANT: Desnoyers,Luc
: APPLICANT: Filvaroff,Ellen
: APPLICANT: Gao,Wel-Qiang
: APPLICANT: Gerritsen,Mary E.
: APPLICANT: Goddard,Andrew
: APPLICANT: Godowski,Paul J.
: APPLICANT: Gurney,Austin L.
: APPLICANT: Sherwood,Steven
: APPLICANT: Smith,Victoria
: APPLICANT: Stewart,Timothy A.
: APPLICANT: Tumas,Daniel
: APPLICANT: Watanabe,Colin K
: APPLICANT: Wood,William
: APPLICANT: Zhang,Zemin
: TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
: FILE REFERENCE: P3330R1C353
: CURRENT APPLICATION NUMBER: US/10/175,746
: CURRENT FILING DATE: 2002-06-19
: Prior Application removed - See File Wrapper or Palm
: NUMBER OF SEQ ID NOS: 550
: SEQ ID NO 8
: LENGTH: 166
: TYPE: PRT
: ORGANISM: Homo Sapien
US-10-175-746-8

Query Match
Best Local Similarity 4.8%; Score 10; DB 9; Length 166;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 89 IKDFMIQGD 98
DB 57 IKDFMIQGD 66

RESULT 13
US-10-176-918-8
```

```

: Sequence 8, Application US/10176918
: Publication No. US20030027275A1
: GENERAL INFORMATION:
: APPLICANT: Baker,Kevin P.
: APPLICANT: Beresini,Maureen
: APPLICANT: Deforge,Laura
: APPLICANT: Desnoyers,Luc
: APPLICANT: Filvaroff,Ellen
: APPLICANT: Gao,Wel-Qiang
: APPLICANT: Gerritsen,Mary E.
: APPLICANT: Goddard,Andrew
: APPLICANT: Godowski,Paul J.
: APPLICANT: Gurney,Austin L.
: APPLICANT: Sherwood,Steven
: APPLICANT: Smith,Victoria
: APPLICANT: Stewart,Timothy A.
: APPLICANT: Tumas,Daniel
: APPLICANT: Watanabe,Colin K
: APPLICANT: Wood,William
: APPLICANT: Zhang,Zemin
: TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
: FILE REFERENCE: P3330R1C288
: CURRENT APPLICATION NUMBER: US/10/176,921
: CURRENT FILING DATE: 2002-06-20
: Prior Application removed - See File Wrapper or Palm
: NUMBER OF SEQ ID NOS: 550
: SEQ ID NO 8
: LENGTH: 166
US-10-176-918-8

Query Match
Best Local Similarity 4.8%; Score 10; DB 9; Length 166;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 89 IKDFMIQGD 98
DB 57 IKDFMIQGD 66

RESULT 14
US-10-176-921-8
: Sequence 8, Application US/10176921
: Publication No. US20030027276A1
: GENERAL INFORMATION:
: APPLICANT: Baker,Kevin P.
: APPLICANT: Beresini,Maureen
: APPLICANT: Deforge,Laura
: APPLICANT: Desnoyers,Luc
: APPLICANT: Filvaroff,Ellen
: APPLICANT: Gao,Wel-Qiang
: APPLICANT: Gerritsen,Mary E.
: APPLICANT: Goddard,Andrew
: APPLICANT: Godowski,Paul J.
: APPLICANT: Gurney,Austin L.
: APPLICANT: Sherwood,Steven
: APPLICANT: Smith,Victoria
: APPLICANT: Stewart,Timothy A.
: APPLICANT: Tumas,Daniel
: APPLICANT: Watanabe,Colin K
: APPLICANT: Wood,William
: APPLICANT: Zhang,Zemin
: TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
: FILE REFERENCE: P3330R1C288
: CURRENT APPLICATION NUMBER: US/10/176,921
: CURRENT FILING DATE: 2002-06-20
: Prior Application removed - See File Wrapper or Palm
: NUMBER OF SEQ ID NOS: 550
: SEQ ID NO 8
: LENGTH: 166
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TYPE: PRT
ORGANISM: Homo Saplen
US-10-176-921-8

Query Match 4.8%; Score 10; DB 9; Length 166;
Best Local Similarity 100.0%; Pred. No. 0.058;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 89 IKDFMIOGCD 98
|||||
DB 57 IKDFMIOGCD 66

RESULT 15

US-10-137-865-8
Sequence 8, Application US/10137865
Publication No. US20030032155A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: DeForge, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Wei-Qiang
APPLICANT: Geritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Sherwood, Steven
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3330RIC154
CURRENT APPLICATION NUMBER: US/10/137,865
CURRENT FILING DATE: 2002-05-03
Prior Application removed - See Palm or File Wrapper
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 8
LENGTH: 166
TYPE: PRT
ORGANISM: Homo Saplen
US-10-137-865-8

Query Match 4.8%; Score 10; DB 9; Length 166;
Best Local Similarity 100.0%; Pred. No. 0.058;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 89 IKDFMIOGCD 98
|||||
DB 57 IKDFMIOGCD 66

Search completed: April 10, 2003, 11:56:23
Job time : 18 secs

GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: April 10, 2003, 11:53:11 ; Search time 20 Seconds
(without alignments) 999.798 Million cell updates/sec

Title: US-09-720-469a-44

Sequence: 208

Sequence: 1 MKVLAALALGASVFFLLP.....VIADCGKIEVEKFAIAKE 208

Scoring table:

Gapop 60.0 , Gapext 60.0

Searched: 283224 seqs, 96134422 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	208	100.0	208	1	CSHUB
2	98	47.1	183	2	S71547
3	98	47.1	216	2	A56861
4	55	26.4	207	2	A40516
5	23	11.1	46	2	S45724
6	19	9.1	165	2	S28020
7	17	8.2	204	2	T21587
8	16	7.7	201	2	T18573
9	16	7.7	212	2	A40047
10	16	7.7	212	2	A54204
11	15	7.2	20	2	S46488
12	15	7.2	171	2	T27371
13	15	7.2	183	2	T18578
14	14	6.7	172	2	T07950
15	14	6.7	215	2	A71261
16	13	6.2	172	2	T50769
17	13	6.2	179	2	A53522
18	13	6.2	205	2	S12324
19	13	6.2	234	2	T49204
20	13	6.2	754	1	TC5314
21	13	6.2	754	1	CSBOAB
22	12	5.8	163	1	CSBOAB
23	12	5.8	163	1	CSBOAB
24	12	5.8	164	1	CSHAC
25	12	5.8	164	1	CSHAC
26	12	5.8	164	1	CSHAC
27	12	5.8	165	1	CSHUA
28	12	5.8	172	2	T27882
29	12	5.8	176	2	T50767

30	12	5.8	176	2	T47724	peptidylprolyl iso
31	12	5.8	179	2	S48018	peptidylprolyl iso
32	12	5.8	201	2	T50837	peptidylprolyl iso
33	12	5.8	201	2	T40819	peptidylprolyl iso
34	12	5.8	201	2	T02489	peptidylprolyl iso
35	12	5.8	204	2	T50838	peptidylprolyl iso
36	12	5.8	260	2	B53422	peptidylprolyl iso
37	12	5.8	347	2	B53522	20k cyclophilin
38	11	5.3	162	1	CSBT	peptidylprolyl iso
39	11	5.3	162	1	CSZPA	peptidylprolyl iso
40	11	5.3	162	1	CSCK	peptidylprolyl iso
41	11	5.3	169	2	S22496	peptidylprolyl iso
42	11	5.3	173	2	T27373	peptidylprolyl iso
43	11	5.3	182	2	S30507	peptidylprolyl iso
44	11	5.3	224	2	T05766	peptidylprolyl iso
45	11	5.3	225	2	S38324	peptidylprolyl iso

ALIGNMENTS

RESULT 1

peptidylprolyl isomerase (EC 5.2.1.8) B precursor (validated) - human
M/Alternate names: cyclophilin B; cyclosporin A-binding protein B; S-cyclophilin
C/Species: Homo sapiens (man)
C/Date: 31-Mar-1992 #sequence revision 31-Mar-1992 #text-change 08-Dec-2000
C/Accession: A39118; A39722; A40515; S65742
R/Price, E.R.; Zydowsky, L.D.; Jin, M.; Baker, C.H.; McKeon, F.D.; Walsh, C.T.
Proc. Natl. Acad. Sci. U.S.A. 88, 1903-1907, 1991
A/Title: Human cyclophilin B: a second cyclophilin gene encodes a peptidyl-prolyl iso
A/Reference number: A39118; MUID:91156714; PMID:2000394
A/Accession: A39118
A/Molecule type: mRNA
A/Residues: 1-208 <PRT>
A/Cross-references: GB:M60857; NID:9181334; PIDN:AAA52150.1; PID:9181335
R/Hassel, K.W.; Glass, J.R.; Godbout, M.; Sutcliffe, J.G.
Mol. Cell. Biol. 11, 3484-3491, 1991
A/Title: An endoplasmic reticulum-specific cyclophilin.
A/Reference number: A39722; MUID:91260697; PMID:1710767
A/Accession: A39722
A/Molecule type: mRNA
A/Residues: 1-208 <HAG>
A/Cross-references: GB:M60457; NID:9181249; PIDN:AAA5733.1; PID:9181250
R/Spik, G.; Haendler, B.; Delmas, O.; Marillier, C.; Chamoux, M.; Maes, P.; Tartar, A
J. Biol. Chem. 266, 10735-10738, 1991
A/Title: A novel secreted cyclophilin-like protein (SCYLP).
A/Reference number: A40515; MUID:91250363; PMID:2040592
A/Accession: A40515
A/Molecule type: mRNA
A/Residues: 1-208 <SPY>
A/Cross-references: GB:M63573; NID:9337998; PIDN:AAA6601.1; PID:9337999
A/Note: the authors' translation begins at an ATG codon in poor context for initiation.
R/Marillier, C.; Allain, F.; Konach, M.; Spik, G.
Biochim. Biophys. Acta 1293, 31-38, 1996
A/Title: Evidence that human milk isolated cyclophilin B corresponds to a truncated
A/Reference number: S65742; MUID:96186273; PMID:8652625
A/Accession: S65742
A/Molecule type: Protein
A/Residues: 26-30;203 <MAR>
A/Experimental source: milk
C/Comment: This protein is distinguished from peptidylprolyl isomerase A by the pres-
C/Comment: This protein binds to and is inhibited by the immunosuppressive drug cyclo-
C/Genetics:
A/Gene: GDB:PP1B
A/Cross-references: GDB:127610; OMIM:123841
A/Map position: 15q21-15q22
C/Function:
A/Description: catalyzes the cis-trans isomerization of peptidylproline peptide bond.
C/Superfamily: peptidylprolyl isomerase; cyclophilin homology
C/Keywords: cis-trans isomerase; cyclosporin A binding; glycoprotein; T-cell
F,1-25/Domain: signal sequence #status Predicted <SIG>

F:26-203/Product: peptidylprolyl isomerase B #status experimental <MAT>
 F:33-197/Domain: cyclophilin homology <CYP>
 F:140/Binding site: carbohydrate (Aan) (covalent) #status predicted

Query Match 100.0%; Score 208; DB 1; Length 208;
 Best Local Similarity 100.0%; Pred. No. 3e-195;
 Matches 208; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 MKVLAALLAGSVFLLLPSPADKKKGRVYKVPDLRIGDEVGRTVIGLGKT 60
 Db 1 MKVLAALLAGSVFLLLPSPADKKKGRVYKVPDLRIGDEVGRTVIGLGKT 60
 Oy 61 VPKTVDFNVALATGEGFGYKSKFRVYIKDPMIOGDFRGGDTGCKSTIGRPPDENE 120
 Db 61 VPKTVDFNVALATGEGFGYKSKFRVYIKDPMIOGDFRGGDTGCKSTIGRPPDENE 120
 Oy 121 KLRHYGGMVSMANAGKDTNGSQFFITVKTAMLDGKHVFGKYLEGMEVVRKVESTKTD 180
 Db 121 KLRHYGGMVSMANAGKDTNGSQFFITVKTAMLDGKHVFGKYLEGMEVVRKVESTKTD 180
 Oy 181 SRDKPLKDVIIADCKRIEVEKPPAIKE 208
 Db 181 SRDKPLKDVIIADCKRIEVEKPPAIKE 208

RESULT 2

S71547
 peptidylprolyl isomerase (EC 5.2.1.8) B, 20.3k - rat
 N:Alternate names: cyclophilin B; PPIASE
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 15-Nov-1996 #sequence_revision 13-Mar-1997 #text_change 16-Jul-1999
 C:Accession: S71547
 R:Ruecknagel, K.P.; Pfeiffer, T.; Rahfeld, J.U.; Schaeffke, M.; Fischer, G.
 submitted to the protein Sequence Database, November 1996
 A:Reference number: S71547
 A:Accession: S71547
 A:Molecule type: protein
 A:Residues: 1-183 <RUE>
 A:Experimental source: liver
 C:Superfamily: peptidylprolyl isomerase; cyclophilin homology
 C:Keywords: cis-trans-isomerase
 F:1-183/Product: peptidylprolyl isomerase, isoform 20.3k #status experimental <MAT>
 F:10-112/Domain: cyclophilin homology <CYP>

Query Match 47.1%; Score 98; DB 2; Length 183;
 Best Local Similarity 100.0%; Pred. No. 7.3e-88;
 Matches 98; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 54 FGLGKTVPTVDNPAALATGEGFGYKSKFRVYIKDPMIOGDFRGGDTGCKSTIGE 113
 Db 29 FGLGKTVPTVDNPAALATGEGFGYKSKFRVYIKDPMIOGDFRGGDTGCKSTIGE 88
 Oy 114 RFPDENKRLHYGPGVSMANAGKDTNGSQFFITVKT 151
 Db 89 RFPDENKRLHYGPGVSMANAGKDTNGSQFFITVKT 126

RESULT 3

A56861
 peptidylprolyl isomerase (EC 5.2.1.8) Cyp-S1 precursor - mouse
 N:Alternate names: cyclophilin B; cyclophilin-S1; cyclosporin A-binding protein
 C:Species: Mus musculus (house mouse)
 C:Date: 05-Jan-1996 #sequence_revision 05-Jan-1996 #text_change 16-Jul-1999
 C:Accession: A56861; B39722; S21835
 R:Schumacher, A.; Schroter, H.; Multhaup, G.; Nordheim, A.
 Biochim. Biophys. Acta 1129, 13-22, 1991
 A:Title: Murine cyclophilin-S1: a variant peptidyl-prolyl isomerase with a putative sign
 A:Reference number: A56861; M01D:92096434; PMID:1756174
 A:Accession: A56861
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-216 <SCH>
 A:Experimental source: teratocarcinoma F9 cells

A>Note: sequence extracted from NCBI backbone (NCBIN:73234, NCBI:73239)
 A>Note: parts of this sequence, including the amino end of the mature protein, were c
 R:Hasel, K.W.; Glass, J.R.; Godbout, M.; Sutcliffe, J.G.
 Mol. Cell. Biol. 11, 3484-3491, 1991
 A:Title: An endoplasmic reticulum-specific cyclophilin.
 A:Reference number: A39722; M01D:91260697; PMID:1710767

A:Accession: B39722
 A:Molecule type: mRNA
 A:Residues: 9-216 <HAS>
 A:Cross-references: GB:M60456; NID:9192864; PIDN:AAA37498.1; PID:9192865
 R:Nordheim, A.
 submitted to the EMBL Data Library, May 1991
 A:Accession: S21835
 A:Reference number: S21835
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 9-216 <NOR>

A:Cross-references: EMBL:X58990; NID:953034; PIDN:CAA1736.1; PID:953035
 C:Comment: This protein is distinguished from peptidylprolyl isomerase A by the prese
 C:Superfamily: peptidylprolyl isomerase; cyclophilin homology
 C:Keywords: cis-trans-isomerase; cyclosporin A binding; endoplasmic reticulum; T-cell
 F:1-33/Domain: signal sequence #status predicted <SIG>
 F:34-216/Product: peptidylprolyl isomerase B #status predicted <MAT>
 F:43-205/Domain: cyclophilin homology <CYP>

Query Match 47.1%; Score 98; DB 2; Length 216;
 Best Local Similarity 100.0%; Pred. No. 8.3e-88;
 Matches 98; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 54 FGLGKTVPTVDNPAALATGEGFGYKSKFRVYIKDPMIOGDFRGGDTGCKSTIGE 113
 Db 62 FGLGKTVPTVDNPAALATGEGFGYKSKFRVYIKDPMIOGDFRGGDTGCKSTIGE 121
 Oy 114 RFPDENKRLHYGPGVSMANAGKDTNGSQFFITVKT 151
 Db 122 RFPDENKRLHYGPGVSMANAGKDTNGSQFFITVKT 159

RESULT 4

A40516
 peptidylprolyl isomerase (EC 5.2.1.8) (S-cyclophilin) precursor - chicken
 C:Species: Gallus gallus (chicken)
 C:Date: 28-Feb-1992 #sequence_revision 28-Feb-1992 #text_change 16-Jul-1999
 C:Accession: A40516
 R:Caroni, P.; Rothenfluh, A.; McClynn, E.; Schneider, C.
 J. Biol. Chem. 266, 10739-10742, 1991
 A:Title: S-cyclophilin. New member of the cyclophilin family associated with the secr
 A:Reference number: A40516; M01D:91250364; PMID:2040593
 A:Accession: A40516
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-207 <CAR>
 A:Cross-references: GB:M63553; NID:9212648; PIDN:AAA49064.1; PID:9212649
 C:Superfamily: peptidylprolyl isomerase; cyclophilin homology
 C:Keywords: cis-trans-isomerase; cyclosporin A binding
 F:34-196/Domain: cyclophilin homology <CYP>

Query Match 26.4%; Score 55; DB 2; Length 207;
 Best Local Similarity 100.0%; Pred. No. 7.9e-46;
 Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 114 RFPDENKRLHYGPGVSMANAGKDTNGSQFFITVKTAMLDGKHVFGKYLEGM 168
 Db 113 RFPDENKRLHYGPGVSMANAGKDTNGSQFFITVKTAMLDGKHVFGKYLEGM 167

RESULT 5

S45724
 peptidylprolyl isomerase (EC 5.2.1.8) B - bovine (fragment)
 N:Alternate names: cyclophilin B
 C:Species: Bos primigenius taurus (cattle)
 C:Date: 25-Dec-1994 #sequence_revision 14-Jul-1995 #text_change 11-Jun-1999
 C:Accession: S45724

R:Galat. A.; Bouet, F.
FEBS Lett. 347, 31-36, 1994
A:Title: Cyclophilin-B is an abundant protein whose conformation is similar to cyclophilin
A:Reference number: S45724; M0ID:94283623; PMID:8013656
A:Accession: S45724
A:Molecule type: protein
A:Residues: 1-46 <GAL>
C:Superfamily: peptidylprolyl isomerase; cyclophilin homology
C:Keywords: cis-trans isomerase; cyclosporin A binding

Query Match 11.1%; Score 23; DB 2; Length 46;
Best Local Similarity 100.0%; Pred. No. 4.2e-15;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 26 DEKKKPKVTYKYFDLRIGDED 48
|||||
Db 1 DEKKKPKVTYKYFDLRIGDED 23

RESULT 6
S28020
peptidylprolyl isomerase (EC 5.2.1.8) - Streptomyces chrysomallus
N:Alternate names: cyclophilin A; cyclosporin A-binding protein
C:Species: Streptomyces chrysomallus
C:Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Jul-1993
R:Pahl, A.; Uehlein, M.; Bang, H.; Schlumbohm, W.; Keller, U.
Mol. Microbiol. 6, 3551-3558, 1992
A:Title: Streptomyces possesses peptidyl-prolyl cis-trans isomerases that strongly resemble
A:Reference number: S28020; M0ID:93116593; PMID:1474897
A:Accession: S28020
A:Molecule type: DNA
A:Residues: 1-165 <PAH>
A:Cross-references: EMBL:215137; NID:946835; PIDN:CA78840.1; PID:946836
C:Superfamily: peptidylprolyl isomerase; cyclophilin homology
C:Keywords: cis-trans isomerase; cyclosporin A binding
F:2-165/Domain: cyclophilin homology <CYP>

Query Match 9.1%; Score 19; DB 2; Length 165;
Best Local Similarity 100.0%; Pred. No. 9.5e-11;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 95 QGSPFTRGDGTGKSTYGE 113
|||||
Db 62 QGSPFTRGDGTGKSTYGE 80

RESULT 7
T21587
peptidylprolyl isomerase (EC 5.2.1.8).F3IC3.1 [similarity] - Caenorhabditis elegans
N:Contains: cyclophilin
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 02-Sep-2000
R:Collage, A.
submitted to the EMBL Data Library, March 1997
A:Reference number: Z19446
A:Accession: T21587
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-204 <MIL>
A:Cross-references: EMBL:292784; PIDN:CA807192.1; GSPDB:GN00019; CESP:F3IC3.1
C:Experimental source: clone F3IC3
C:Genetics:
A:Gene: CESP:F3IC3.1
A:Map position: 1
A:Introns: 69/3
C:Superfamily: peptidylprolyl isomerase; cyclophilin homology
C:Keywords: cis-trans isomerase
F:28-190/Domain: cyclophilin homology <CYP>

Query Match 8.2%; Score 17; DB 2; Length 204;
Best Local Similarity 100.0%; Pred. No. 1e-08;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 91 DFMIOGDFTRGDGTGG 107
|||||
Db 84 DFMIOGDFTRGDGTGG 100

RESULT 8
T18573
peptidylprolyl isomerase (EC 5.2.1.8) precursor - Caenorhabditis elegans
N:Alternate names: cyclophilin
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 02-Sep-2000
C:Accession: T18573; T16351
R:Page, A.P.
submitted to the EMBL Data Library, May 1995
A:Reference number: Z18981
A:Accession: T18573
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-201 <PAG>
A:Cross-references: EMBL:U27354; PIDN:AAC47124.1; GSPDB:GN00021; CESP:cyp-6
A:Experimental source: strain N2
R:Raich, A.
submitted to the EMBL Data Library, March 1996
A:Description: The sequence of C. elegans cosmid F42G9.
A:Reference number: Z18498
A:Accession: T16351
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-201 <TAI>
A:Cross-references: EMBL:U00051; NID:q1216305; PID:9485120; PIDN:AAA91355.1; CESP:F42
A:Experimental source: strain Bristol N2
C:Genetics:
A:Gene: CESP:cyp-6
A:Map position: 3
A:Introns: 66/3
C:Superfamily: peptidylprolyl isomerase; cyclophilin homology
C:Keywords: cis-trans isomerase
F:25-187/Domain: cyclophilin homology <CYP>

Query Match 7.7%; Score 16; DB 2; Length 201;
Best Local Similarity 100.0%; Pred. No. 9.5e-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 92 FMIQSGDFTRGDGTGG 107
|||||
Db 82 FMIQSGDFTRGDGTGG 97

RESULT 9
AA0047
peptidylprolyl isomerase (EC 5.2.1.8) (cyclophilin C) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 16-Jul-1999
C:Accession: AA0047
R:Friedman, J.; Weisman, I.
Cell 66, 799-806, 1991
A:Title: Two cytoplasmic candidates for immunophilin action are revealed by affinity
A:Reference number: AA0047; M0ID:91347379; PMID:1652374
A:Accession: AA0047
A:Molecule type: DNA
A:Residues: 1-212 <FRI>
A:Cross-references: GB:M74227; NID:q192898; PIDN:AAA37511.1; PID:q192899
A:Comment: This protein binds the immunosuppressive drug cyclosporin A.
C:Superfamily: peptidylprolyl isomerase; cyclophilin homology
C:Keywords: cis-trans isomerase; cyclosporin A binding
F:37-199/Domain: cyclophilin homology <CYP>

Query Match 7.7%; Score 16; DB 2; Length 212;
Best Local Similarity 100.0%; Pred. No. 9.9e-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 85 FHRVTKDFMIOGDEF 100
 DB 87 FHRVTKDFMIOGDEF 102

RESULT 10

A54204
 peptidylprolyl isomerase (EC 5.2.1.8) C precursor - human
 N:Alternate names: cyclophilin C
 C:Species: Homo sapiens (man)
 C:Date: 22-Oct-1994 #sequence_revision 18-Nov-1994 #text_change 16-Jul-1999
 C:Accession: A54204
 R:Schneider, H.; Charara, N.; Schmitz, R.; Wehrli, S.; Mikol, V.; Zurini, M.G.; Quesniau
 Biochemistry 33, 8218-8224, 1994
 A:Title: Human cyclophilin C: primary structure, tissue distribution, and determination
 A:Reference number: A54204; MUID:94304830; PMID:8031755
 A:Accession: A54204
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-212 <SCH>
 A:Cross-references: GB:S71018; NID:9547303; PIDN:AAB31350.1; PID:9547304
 A:Experimental source: kidney
 A:Note: sequence extracted from NCBI backbone (NCBIN:149387, NCBI:149388)
 C:Genetics:
 A:Gene: GDB:PPIC
 A:Cross-references: GDB:136196; OMIM:123842
 A:Map position: 15q21-15q22
 C:Superfamily: peptidylprolyl isomerase; cyclophilin homology
 C:Keywords: cis-trans-isomerase; cyclosporin A binding
 F:37-199/Domain: cyclophilin homology <CYP>

Query Match 7.7%; Score 16; DB 2; Length 212;
 Best Local Similarity 100.0%; Pred. No. 9.9e-08;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 83 SKFHRVTKDFMIOGCD 98
 DB 85 SKFHRVTKDFMIOGCD 100

RESULT 11

S46488
 peptidylprolyl isomerase (EC 5.2.1.8) - bovine (fragment)
 N:Alternate names: peptidylprolyl cis-trans-isomerase
 N:Contents: cyclophilin
 C:Species: Bos primigenius taurus (cattle)
 C:Date: 15-Jul-1995 #sequence_revision 26-Jul-1996 #text_change 02-Sep-2000
 C:Accession: S46488
 R:Bose, S.; Muecke, M.; Freedman, R.B.
 Biochem. J. 300, 871-875, 1994
 A:Title: The characterization of a cyclophilin-type peptidyl prolyl cis-trans-isomerase
 A:Reference number: S46488; MUID:94280416; PMID:8010972
 A:Accession: S46488
 A:Molecule type: protein
 A:Residues: 1-20 <BOS>
 C:Superfamily: peptidylprolyl isomerase; cyclosporin A binding
 C:Keywords: cis-trans-isomerase; cyclosporin A binding

Query Match 7.2%; Score 15; DB 2; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.4e-07;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 31 GPKVTKVTFDLRIG 45
 DB 6 GPKVTKVTFDLRIG 20

RESULT 12

T27371
 peptidylprolyl isomerase (EC 5.2.1.8) Y75B12B.2 [similarity] - Caenorhabditis elegans
 N:Contents: cyclophilin
 C:Species: Caenorhabditis elegans
 C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 02-Sep-2000

C:Accession: T27371

R:White, S.

submitted to the EMBL Data Library, October 1998

A:Reference number: 220360

A:Accession: T27371

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-171 <MII>

A:Cross-references: EMBL:AL032663; PIDN:CAA21760.1; GSPDB:GN00023; CESP:Y75B12B.2

A:Experimental source: clone Y75B12B

C:Genetics:

A:Gene: CESP:Y75B12B.2

A:Map position: 5

A:Introns: 23/3; 107/3

C:Superfamily: peptidylprolyl isomerase; cyclophilin homology

C:Keywords: cis-trans-isomerase

F:3-171/Domain: cyclophilin homology <CYP>

Query Match 7.2%; Score 15; DB 2; Length 171;
 Best Local Similarity 100.0%; Pred. No. 7.9e-07;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 148 TVKTAWLDKRVFEG 162
 DB 123 TVKTAWLDKRVFEG 137

RESULT 13

T18578
 peptidylprolyl isomerase (EC 5.2.1.8) cyp-11 [similarity] - Caenorhabditis elegans
 N:Contents: cyclophilin
 C:Species: Caenorhabditis elegans
 C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 08-Sep-2000
 C:Accession: T18578; T24269
 R:Page, A.P.; MacIven, K.
 submitted to the EMBL Data Library, August 1995
 A:Reference number: T18578
 A:Accession: T18578
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-183 <PAC>
 A:Cross-references: EMBL:U34955; PIDN:AAC47115.1
 A:Experimental source: strain Bristol N2
 R:Sim, M.
 submitted to the EMBL Data Library, October 1995
 A:Reference number: T19867
 A:Accession: T24269
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-183 <MII>
 A:Cross-references: EMBL:Z66499; PIDN:CAA91297.1; GSPDB:GN00020; CESP:T01B7.4
 A:Experimental source: clone T01B7
 C:Genetics:
 A:Gene: CESP:cyp-11
 A:Map position: 2
 A:Introns: 34/3; 87/3; 148/1
 C:Superfamily: peptidylprolyl isomerase; cyclophilin homology
 C:Keywords: cis-trans-isomerase
 F:16-183/Domain: cyclophilin homology <CYP>

Query Match 7.2%; Score 15; DB 2; Length 183;
 Best Local Similarity 100.0%; Pred. No. 8.3e-07;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 85 FHRVTKDFMIOGDF 99
 DB 71 FHRVTKDFMIOGDF 85

RESULT 14

T07950
 peptidylprolyl isomerase (EC 5.2.1.8) 1 - Chlamydomonas reinhardtii
 N:Alternate names: cyclophilin 1; peptidyl-prolyl cis-trans isomerase

C:Species: Chlamydomonas reinhardtii
 C:Date: 21-May-1999 #sequence_revision 21-May-1999 #text_change 08-Oct-1999
 C:Accession: T07950
 R:Somanchi, A.; Handley, E.R.; Moroney, J.V.
 submitted to the EMBL Data Library, March 1998
 A:Description: Identification of a cyclophilin cDNA from Chlamydomonas reinhardtii.
 A:Reference number: 216241
 A:Accession: T07950
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-172 <SDM>
 A:Cross-References: EMBL:AF052206; NID:g2959711; PIDN:AAC05639.1; PID:g2959712
 C:Genetics:
 A:Gene: cyp1
 C:Superfamily: peptidylprolyl isomerase; cyclophilin homology
 C:Keywords: cis-trans-isomerase; cyclosporin A binding
 F:3-171/Domain: cyclophilin homology <CYP>

Query Match 6.7%; Score 14; DB 2; Length 172;
 Best Local Similarity 100.0%; Pred. No. 7.5e-06;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 151 TAMLGKHYVFGKV 164
 |||||
 Db 126 TAMLGKHYVFGKV 139

RESULT 15

A71261
 peptidylprolyl isomerase (EC 5.2.1.8) TP0947 [similarity] - syphilis spirochete
 N:Contains: cyclophilin
 C:Species: Treponema pallidum subsp. pallidum (syphilis spirochete)
 C:Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 08-Sep-2000
 C:Accession: A71261
 R:Fraser, C.M.; Morris, S.J.; Weinstock, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Gwin
 Tson, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Utterback, T.; MCD
 Uney, L.; Weidman, J.; Smith, H.O.; Venter, J.C.
 A:Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete.
 A:Reference number: A71250; MUID:98332770; PMID:9665876
 A:Accession: A71261
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-215 <COL>
 A:Cross-References: GB:AE001263; GB:AE000520; NID:g3323266; PIDN:AAC65904.1; PID:g332326
 A:Experimental source: strain Nichols
 C:Genetics:
 A:Gene: TP0947
 C:Superfamily: peptidylprolyl isomerase; cyclophilin homology
 C:Keywords: cis-trans-isomerase
 F:34-206/Domain: cyclophilin homology <CYP>

Query Match 6.7%; Score 14; DB 2; Length 215;
 Best Local Similarity 100.0%; Pred. No. 9e-06;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 85 FHRVTKDFMIOGD 98
 |||||
 Db 89 FHRVTKDFMIOGD 102

Search completed: April 10, 2003, 11:55:39
 Job time : 21 secs

GenCore version 5.1.4-p5.4578
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OM protein - protein search, using sw model

Run on: April 10, 2003, 11:52:26 ; Search time 12 Seconds

(without alignments)
718.923 Million cell updates/sec

Title: US-09-720-469a-44

Perfect score: 208
Sequence: 1 MKVLLAALALGSGVFLLLP.....VLIADCGKIEVEKPAFAKE 208

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 112892 seqs, 41476328 residues

Word size : 0

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	208	100.0	208	1	CYPB_HUMAN
2	98	47.1	208	1	P23284 homo sapien
3	77	37.0	208	1	P24369 mus musculu
4	63	30.3	208	1	P80311 bos taurus
5	55	26.4	207	1	P23368 rattus norv
6	19	9.1	165	1	P24367 gallus gall
7	17	8.2	204	1	Q06118 streptomyce
8	16	7.7	201	1	P52013 caenorhabdi
9	16	7.7	212	1	P52014 caenorhabdi
10	16	7.7	212	1	P45877 homo sapien
11	15	7.2	171	1	P30412 mus musculu
12	15	7.2	183	1	P52015 caenorhabdi
13	14	6.7	215	1	P52018 caenorhabdi
14	13	6.2	150	1	O66105 treponema p
15	13	5.8	205	1	P34867 allium cepa
16	12	5.8	163	1	P23285 saccharomyc
17	12	5.8	163	1	P04374 bos taurus
18	12	5.8	163	1	P14851 cricetus
19	12	5.8	163	1	P17742 mus musculu
20	12	5.8	163	1	P10111 rattus norv
21	12	5.8	171	1	O00060 uromyces fa
22	12	5.8	171	1	P05092 homo sapien
23	12	5.8	172	1	P52010 caenorhabdi
24	12	5.8	260	1	O49886 lupinus lut
25	11	5.3	161	1	P34791 arabidopsis
26	11	5.3	162	1	P14871 saccharomyc
27	11	5.3	162	1	P22011 candida alb
28	11	5.3	169	1	P18253 schizosacch
29	11	5.3	173	1	P35627 arabidopsis
30	11	5.3	182	1	P52011 caenorhabdi
31	11	5.3	225	1	P25719 saccharomyc
32	11	5.3	370	1	P5176 saccharomyc
33	11	5.3	370	1	P26862 bos taurus
					Q08752 homo sapien

ALIGNMENTS

RESULT 1	CYPB_HUMAN	STANDARD	PRT	208 AA.	
AC	P23284:				P14088 echinococcu
DT	01-NOV-1991 (Rel. 20, Created)				P54985 Blattella g
DT	01-NOV-1991 (Rel. 41, Last sequence update)				P31791 hemitelectro
DT	15-JUN-2002 (Rel. 41, Last annotation update)				Q97366 homo sapien
DE	Peptidyl-prolyl cis-trans isomerase B precursor (EC 5.2.1.8) (PPIase)				Q960W5 mus musculu
DE	(Rotamase) (Cyclophilin B) (S-cyclophilin) (SCYLP) (CYP-S1).				P24525 brassica na
GN	PP1B OR CYPB.				P34790 arabidopsis
OS	Homo sapiens (Human).				Q39613 catharantus
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				P21569 zea mays (m
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.				P52009 caenorhabdi
OX	NCBI_TaxID=9606;				Q99kr7 mus musculu
RN					P29117 rattus norv
RP	SEQUENCE FROM N.A., AND SEQUENCE OF 26-40.				
RX	MEDLINE=91156714; PubMed=2000394;				
RA	Price E.R., Zydowsky L.D., Jin M., Hunter C.H., McKeon F.D.,				
RA	Walsh C.T.;				
RT	"Human cyclophilin B: a second cyclophilin gene encodes a peptidyl-				
RT	prolyl isomerase with a signal sequence.";				
RL	Proc. Natl. Acad. Sci. U.S.A. 88:1903-1907(1991).				
RN					
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=91250363; PubMed=2040592;				
RA	Spik G., Haendler B., Delmas O., Marillier C., Chamoux M., Maes P.,				
RA	Tartat A., Montreuil J., Stedman K., Kocher H.P., Keller R.,				
RA	Hiestand P.C., Movva N.R.;				
RT	"A novel secreted cyclophilin-like protein (SCYLP)."				
RL	J. Biol. Chem. 266:10735-10738(1991).				
RN					
RP	SEQUENCE OF 2-208 FROM N.A.				
RX	MEDLINE=91260697; PubMed=1710767;				
RA	Hasel K.W., Glass J.R., Godbout M., Sutcliffe J.G.;				
RT	"An endoplasmic reticulum-specific cyclophilin.";				
RL	Mol. Cell. Biol. 11:3484-3491(1991).				
RN					
RP	SEQUENCE OF 64-76 AND 151-157.				
RX	MEDLINE=91162043; PubMed=1286667;				
RA	Rasmussen H.H., van Damme J., Puype M., Gesser B., Celis J.E.,				
RA	Vandekerckhove J.;				
RT	"Microsequences of 145 proteins recorded in the two-dimensional gel				
RL	protein database of normal human epidermal keratinocytes.";				
RN	Electrophoresis 13:960-969(1992).				
RN					
RP	SUBCELLULAR LOCATION.				
RX	MEDLINE=92112948; PubMed=1530944;				
RA	Arber S., Krause K.-H., Caroni P.;				
RT	"S-cyclophilin is retained intracellularly via a unique COOH-terminal				
RT	sequence and colocalizes with the calcium storage protein				
RL	calreticulin.";				
RN	J. Cell Biol. 116:113-125(1992).				
RN					
RP	X-RAY CRYSTALLOGRAPHY (1.85 ANGSTROMS).				
RX	MEDLINE=94255495; PubMed=8197205;				
RA	Mikol V., Kallen J., Walkinshaw M.D.;				

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RT *X-ray structure of a cyclophilin B/cyclosporin complex: comparison
RT with cyclophilin A and delineation of its calcineurin-binding
RT domain."
RL Proc. Natl. Acad. Sci. U.S.A. 91:5183-5186(1994).
CC -1- FUNCTION: Pripases accelerate the folding of proteins. It catalyzes
CC the cis-trans isomerization of proline imidic peptide bonds in
CC oligopeptides.
CC -1- CATALYTIC ACTIVITY: Peptidylproline (omega-180) = peptidylproline
CC (omega-0).
CC -1- ENZYME REGULATION: CYCLOSPORIN A (CSA) INHIBITS CYPB.
CC -1- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.
CC -1- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PRIPASE FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: M60857; AAA52150.1; -
DR EMBL: M63573; AAA36601.1; ALT_INIT.
DR EMBL: M60457; AAA35733.1; -
DR PIR: A39118; CSHUB.
DR PIR: A40515; A40515.
DR PDB: 1CYN: 29-JAN-96.
DR SWISS-2DPAGE: P23284; HUMAN.
DR Aarhus/Genent-2DPAGE: 117; NEPHEB.
DR Genew: HGNC:9255; PP1B.
DR MIM: 123841; -
DR InterPro: IPR002130; CSA_Priase.
DR Pfam: PF00160; pro_Isoomerase; 1.
DR PRINTS: PR00153; CSAPRISMASE.
DR PROSITE: PS00170; CSA_Priase_1; 1.
DR PROSITE: PS50072; CSA_Priase_2; 1.
DR Cyclosporin: Isoomerase; Rotamase; Signal; Endoplasmic reticulum;
KW Multigene family; 3D-structure.
FT SIGNAL 1 25
FT CHAIN 26 208 PEPTIDYL-PROLYL CIS-TRANS ISOMERASE B.
FT SITE 199 208 PREVENT SECRETION FROM ER.
SQ SEQUENCE 208 AA; 22742 MW; A814481B7EBD4579 CRC64;

Query Match 100.0%; Score 208; DB 1; Length 208;
Best Local Similarity 100.0%; Pred. No. 8.5e-184;
Matches 208; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MVLVLAALINGVFELLIGPSAADKKKGPVTKYVFEDLRIGDEVDGRTIGLSEKT 60
DB 1 MVLVLAALINGVFELLIGPSAADKKKGPVTKYVFEDLRIGDEVDGRTIGLSEKT 60
QY 61 VKRTVDNFVALATGEKGFYKNSKFRHIVDFMIQCGDFTREDGTGKSTYGERPPDENF 120
DB 61 VKRTVDNFVALATGEKGFYKNSKFRHIVDFMIQCGDFTREDGTGKSTYGERPPDENF 120
QY 121 KLRHVGPGWVSMANAGKDTNGSOFITTVKTATLDDKHHVFGVLEGEVYKRVSESTTD 180
DB 121 KLRHVGPGWVSMANAGKDTNGSOFITTVKTATLDDKHHVFGVLEGEVYKRVSESTTD 180
QY 181 SRDKPLKDVIIADCGKIEVEKFAIAKE 208
DB 181 SRDKPLKDVIIADCGKIEVEKFAIAKE 208

RESULT 2
CYPB_MOUSE STANDARD: PRT; 208 AA.
AC P24369;
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-MAR-1992 (Rel. 21, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Peptidyl-prolyl cis-trans isomerase B precursor (EC 5.2.1.8) (Ppiase)
DE (Rotamase) (Cyclophilin B) (S-cyclophilin) (SCYPB) (CYP-S1).

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GN PP1B.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX MBL_TaxID-10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-91260697; PubMed-1710767;
RA Hasel K.W., Glass J.R., Godbout M., Sutcliffe J.G.;
RT "An endoplasmic reticulum-specific cyclophilin."
RL Mol. Cell. Biol. 11:3484-3491(1991).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE-92096454; PubMed-1756174;
RA Schumacher A., Schroeter H., Mulhaup G., Nordheim A.;
RT "Murine cyclophilin-S1: a variant peptidyl-prolyl isomerase with a
RT putative signal sequence expressed in differentiating f9 cells."
RL Biochim. Biophys. Acta 1129:13-22(1991).
CC -1- FUNCTION: Pripases accelerate the folding of proteins. It catalyzes
CC the cis-trans isomerization of proline imidic peptide bonds in
CC oligopeptides.
CC -1- CATALYTIC ACTIVITY: Peptidylproline (omega-180) = peptidylproline
CC (omega-0).
CC -1- ENZYME REGULATION: CYCLOSPORIN A (CSA) INHIBITS CYPB.
CC -1- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen (By similarity).
CC -1- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PRIPASE FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: M60456; AAA37498.1; -
DR EMBL: X58990; CAA41736.1; -
DR PIR: B39722; B39722.
DR PIR: S21835; S21835.
DR HSSP: P23284; 1CYN.
DR MGD: MGI:97750; Pp1b.
DR InterPro: IPR002130; CSA_Priase.
DR Pfam: PF00160; pro_Isoomerase; 1.
DR PRINTS: PR00153; CSAPRISMASE.
DR PROSITE: PS00170; CSA_Priase_1; 1.
DR PROSITE: PS50072; CSA_Priase_2; 1.
DR Cyclosporin: Isoomerase; Rotamase; Signal; Endoplasmic reticulum;
KW Multigene family.
FT SIGNAL 1 25 BY SIMILARITY.
FT CHAIN 26 208 PEPTIDYL-PROLYL CIS-TRANS ISOMERASE B.
FT SITE 199 208 PREVENT SECRETION FROM ER
FT (BY SIMILARITY).
SQ SEQUENCE 208 AA; 22713 MW; 48BDF3AE40BD3A7 CRC64;

Query Match 47.1%; Score 98; DB 1; Length 208;
Best Local Similarity 100.0%; Pred. No. 9.8e-83;
Matches 98; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 54 FGLGKTYVPKTVDNFVALATGEKGFYKNSKFRHIVKIPMIQCGDFTRGDGTGKSTYGE 113
DB 54 FGLGKTYVPKTVDNFVALATGEKGFYKNSKFRHIVKIPMIQCGDFTRGDGTGKSTYGE 113
QY 114 RPPDENFKLRHVGPGWVSMANAGKDTNGSOFITTVKT 151
DB 114 RPPDENFKLRHVGPGWVSMANAGKDTNGSOFITTVKT 151

RESULT 3
CYPB_BOVIN STANDARD: PRT; 208 AA.
AC P80311;
DT 01-JUN-1994 (Rel. 29, Created)

```

DT 01-NOV-1995 (Rel. 32, last sequence update)
 DT 15-JUN-2002 (Rel. 41, last annotation update)
 DE Peptidyl-prolyl cis-trans isomerase B precursor (EC 5.2.1.8) (PPIase)
 DE (Rotamase) (Cyclophilin B) (S-cyclophilin) (SCYLP).
 GN PPIB.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 ON NCBI_TaxID=9913;
 RX [1]
 RP SEQUENCE FROM N.A.
 RA TISSUE=Oterus.
 RA Carrello A., Mark P.J., House A.K., Ratajezak T.;
 RA Submitted (Jan-1993) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE OF 26-71.
 RC TISSUE=Brain;
 RX MEDLINE=94283623; PubMed=8013656;
 RA Galat A., Bouet F.;
 RT "Cyclophilin-B is an abundant protein whose conformation is similar
 RT to cyclophilin-A.";
 RL FEBS Lett. 347:31-36(1994).
 RN [3]
 RP SEQUENCE OF 26-45.
 RX MEDLINE=94280416; PubMed=8010972;
 RA Bose S., Muecke M., Freedman R.B.;
 RT "The characterization of a cyclophilin-type peptidyl prolyl
 RT cis-trans isomerase from the endoplasmic-reticulum lumen.";
 RL Biochem. J. 300:871-875(1994).
 CC -1- FUNCTION: PPIases accelerate the folding of proteins. It catalyzes
 CC the cis-trans isomerization of proline imidic peptide bonds in
 CC oligopeptides.
 CC -1- CATALYTIC ACTIVITY: Peptidylproline (omega-180) = peptidylproline
 CC (omega-0).
 CC -1- ENZYME REGULATION: CYCLOSPORIN A (CSA) INHIBITS CYPB.
 CC -1- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.
 CC -1- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY.
 CC -----
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 CC -----
 DR EMBL: D14073; BAA03158.1; .
 DR HSSP: P23284; ICYN.
 DR InterPro: IPR002130; CSA_PPIase.
 DR Pfam: PF00160; pro_isomerase; 1.
 DR PRINTS: PR00153; CSAPPISMRASP.
 DR PROSITE: PS00170; CSA_PPIASE_1; 1.
 DR PROSITE: PS50072; CSA_PPIASE_2; 1.
 DR Cyclosporin; Isomerase; Rotamase; Signal; Endoplasmic reticulum;
 KW Multigene family.
 FT SIGNAL 1 25
 FT CHAIN 1 208
 FT SITE 199 208 PREVENT SECRETION FROM ER.
 FT CONFLICT 30 30 K -> G (IN REF. 3).
 SQ SEQUENCE 208 AA; 22701 MW; 0097C88289AFC6276 CRC64;

Query Match 37.0%; Score 77; DB 1; Length 208;
 Best Local Similarity 100.0%; Pred. No. 1.9e-63;
 Matches 77; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 83 SKFHRVAKDFMIQGGDTRDGTGKSIYGERPPDENFKLKHGPGVSMANACKDINGS 142
 DB 83 SKFHRVAKDFMIQGGDTRDGTGKSIYGERPPDENFKLKHGPGVSMANACKDINGS 142
 OY 143 QFFITVKTAMLDGKHV 159
 DB 143 QFFITVKTAMLDGKHV 159

RESULT 4
 ID CYPB_RAT STANDARD; PRT; 208 AA.
 AC P24368;
 DT 01-MAR-1992 (Rel. 21, Created)
 DT 01-MAR-1992 (Rel. 21, Last sequence update)
 DE 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Peptidyl-prolyl cis-trans isomerase B precursor (EC 5.2.1.8) (PPIase)
 DE (Rotamase) (Cyclophilin B) (S-cyclophilin) (SCYLP) (CYP-51).
 GN PPIB.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 ON NCBI_TaxID=10116;
 RX [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=90300692; PubMed=2194066;
 RA Iwai N., Inagami T.;
 RT "Molecular cloning of a complementary DNA to rat cyclophilin-like
 RT protein mRNA.";
 RL Kidney Int. 37:1460-1465(1990).
 RN [2]
 RP REVISIONS TO C-TERMINUS.
 RX MEDLINE=92112948; PubMed=1530944;
 RA Arber S., Krause K.-H., Caroni P.;
 RT "S-cyclophilin is retained intracellularly via a unique COOH-terminal
 RT sequence and colocalizes with the calcium storage protein
 RT calreticulin.";
 RL J. Cell Biol. 116:113-125(1992).
 CC -1- FUNCTION: PPIases accelerate the folding of proteins. It catalyzes
 CC the cis-trans isomerization of proline imidic peptide bonds in
 CC oligopeptides.
 CC -1- CATALYTIC ACTIVITY: Peptidylproline (omega-180) = peptidylproline
 CC (omega-0).
 CC -1- ENZYME REGULATION: CYCLOSPORIN A (CSA) INHIBITS CYPB.
 CC -1- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen (By similarity).
 CC -1- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY.
 CC -----
 CC HSSP: P23284; ICYN.
 DR InterPro: IPR002130; CSA_PPIase.
 DR Pfam: PF00160; pro_isomerase; 1.
 DR PRINTS: PR00153; CSAPPISMRASP.
 DR PROSITE: PS00170; CSA_PPIASE_1; 1.
 DR PROSITE: PS50072; CSA_PPIASE_2; 1.
 DR Cyclosporin; Isomerase; Rotamase; Signal; Endoplasmic reticulum;
 KW Multigene family.
 FT SIGNAL 1 25
 FT CHAIN 1 208
 FT SITE 199 208 PREVENT SECRETION FROM ER
 FT CONFLICT 199 208 BY SIMILARITY.
 SQ SEQUENCE 208 AA; 23025 MW; 76D12AC3427FEF32 CRC64;

Query Match 30.3%; Score 63; DB 1; Length 208;
 Best Local Similarity 100.0%; Pred. No. 1.4e-50;
 Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 89 IKDFMIQGGDTRDGTGKSIYGERPPDENFKLKHGPGVSMANACKDINGSQFFITTT 148
 DB 89 IKDFMIQGGDTRDGTGKSIYGERPPDENFKLKHGPGVSMANACKDINGSQFFITTT 148
 OY 149 VKT 151
 DB 149 VKT 151

RESULT 5
 ID CYPB_CHICK STANDARD; PRT; 207 AA.
 AC P24367;
 DT 01-MAR-1992 (Rel. 21, Created)
 DT 01-MAR-1992 (Rel. 21, Last sequence update)
 DE 15-JUN-2002 (Rel. 41, Last annotation update)

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DE Peptidyl-prolyl cis-trans isomerase B precursor (EC 5.2.1.8) (PPIase)
DE (Rotamase) (Cyclophilin B) (S-cyclophilin) (SCYP).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
ON NCBI_TaxID=9031;
RN [1]
RP MEDLINE=91250364; PubMed=2040593;
RA Caroni P., Rottemblut A., McGlynn E., Schneider C.;
RT "S-cyclophilin. New member of the cyclophilin family associated with
RT the secretory pathway."
RT J. Biol. Chem. 266:10739-10742(1991).
CC -1- FUNCTION: PPIases accelerate the folding of proteins. It catalyzes
CC the cis-trans isomerization of proline imide peptide bonds in
CC oligopeptides.
CC -1- CATALYTIC ACTIVITY: Peptidylproline (omega-180) = peptidylproline
CC (omega-0).
CC -1- ENZYME REGULATION: CYCLOSPORIN A (CSA) INHIBITS CYPB.
CC -1- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen (By similarity).
CC -1- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY.
CC -----
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CC -----
DR EMBL: M63553; AAA49064.1; -.
DR PIR: A40516; A40516.
DR HSP: P23284; ICYN.
DR InterPro: IPR002130; CSA_PPIase.
DR Pfam: PF00160; pro_isomerase; 1.
DR PRINTS: PR00153; CSAPPISMRASE.
DR PROSITE: PS00170; CSA_PPIASE_1; 1.
DR PROSITE: PS0072; CSA_PPIASE_2; 1.
DR Cyclosporin; Isomerase; Rotamase; Signal; Endoplasmic reticulum;
KW Multigene family.
FT SIGNAL 1 24
FT CHAIN 25 207
FT SITE 198 207
FT ST 207
SQ SEQUENCE 207 AA; 22413 MW; D9C0C2E528E25B59 CRC64;
Query Match 26.4%; Score 55; DB 1; Length 207;
Best Local Similarity 100.0%; Pred. No. 3,1e-43;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 114 RPDPENFKLHYGPGVSNANAGKDTNGSQFITTVKAMLDGKHYVFGKYLQGM 168
DB 113 RPPDENFKLHYGPGVSNANAGKDTNGSQFITTVKAMLDGKHYVFGKYLQGM 167
RESULT 6
PRT_STRCH STANDARD; PRT: 165 AA.
AC Q06118;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Peptidyl-prolyl cis-trans isomerase (EC 5.2.1.8) (PPIase) (Rotamase)
DE (Cyclophilin homolog).
OS Streptomyces chrysomallus.
OC Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae;
OC Actinomycetales; Streptomycinae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1899;
RN [1]
RP SEQUENCE FROM N.A. AND SEQUENCE OF 4-41.
RC STRAIN=ATCC 11523;
RX MEDLINE=93116593; PubMed=1474897;

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RA Pahl A., Uehlein M., Bang H., Schlumbohm W., Keller U.;
RT "Streptomycetes possess peptidyl-prolyl cis-trans isomerases that
RT strongly resemble cyclophilins from eukaryotic organisms."
RT Mol. Microbiol. 6:3551-3558(1992).
CC -1- FUNCTION: PPIases accelerate the folding of proteins. It catalyzes
CC the cis-trans isomerization of proline imide peptide bonds in
CC oligopeptides.
CC -1- CATALYTIC ACTIVITY: Peptidylproline (omega-180) = peptidylproline
CC (omega-0).
CC -1- ENZYME REGULATION: BINDS CYCLOSPORIN A (CSA). CSA MEDIATES SOME
CC OF ITS EFFECTS VIA AN INHIBITORY ACTION ON PPIASE.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY.
CC -----
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CC -----
DR EMBL: Z15137; CAA78840.1; -.
DR PIR: S28020; S28020.
DR HSP: P05092; 2CPL.
DR InterPro: IPR002130; CSA_PPIase.
DR Pfam: PF00160; pro_isomerase; 1.
DR PRINTS: PR00153; CSAPPISMRASE.
DR PROSITE: PS00170; CSA_PPIASE_1; 1.
DR PROSITE: PS0072; CSA_PPIASE_2; 1.
KW Cyclosporin; Isomerase; Rotamase.
SQ SEQUENCE 165 AA; 17716 MW; 2CFIDF725CD6FA7D CRC64;
Query Match 9.1%; Score 19; DB 1; Length 165;
Best Local Similarity 100.0%; Pred. No. 3,2e-10;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 95 QGGDFTRGDTGSGSYGE 113
DB 62 QGGDFTRGDTGSGSYGE 80
RESULT 7
CYP5_CABEL STANDARD; PRT: 204 AA.
AC P52013;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Peptidyl-prolyl cis-trans isomerase 5 (EC 5.2.1.8) (PPIase) (Rotamase)
DE (Cyclophilin-5).
OS Ctenorhabdittis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabdittida; Rhabdittidae.
OC Rhabdittidae; Peloderinae; Ctenorhabdittis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX MEDLINE=96276416; PubMed=8694762;
RA Page A.P., MacIver K., Hengartner M.O.;
RT "Cloning and biochemical characterization of the cyclophilin
RT homologues from the free-living nematode Ctenorhabdittis elegans."
RT Biochem. J. 317:179-185(1996).
DE Peptidyl-prolyl cis-trans isomerase 5 (EC 5.2.1.8) (PPIase) (Rotamase)
DE (Cyclophilin-5).
CC -1- FUNCTION: PPIases accelerate the folding of proteins. It catalyzes
CC the cis-trans isomerization of proline imide peptide bonds in
CC oligopeptides.
CC -1- CATALYTIC ACTIVITY: Peptidylproline (omega-180) = peptidylproline
CC (omega-0).
CC -1- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY.
CC -----
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DR EMBL: U31948; AAC47126.1; -
 DR HSSP: P23284; ICYN.
 DR InterPro: IPR002130; CSA_PPIase.
 DR Pfam: PF00160; PRO_Isoomerase; 1.
 DR PRINTS: PS00153; CSAPPISMRASE.
 DR PROSITE: PS00170; CSA_PPIASE.1; 1.
 DR PROSITE: PS50072; CSA_PPIASE.2; 1.
 DR Isoomerase; Rotomase; Multigene family.
 SQ SEQUENCE 204 AA; 22366 MW; 22ABB39AD1127BAA CRC64;

Query Match 8.28; Score 17; DB 1; Length 204;
 Best Local Similarity 100.0%; Pred. No. 2.5e-08;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 91 DFMIOGDFTRDGTGG 107
 Db 84 DFMIOGDFTRDGTGG 100
 |||||

RESULT 8
 CYP6_CAEEL STANDARD; PRT; 201 AA.
 ID CYP6_CAEEL
 AC P52014;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Peptidyl-prolyl cis-trans isomerase 6 precursor (EC 5.2.1.8) (PPIase)
 DE (Rotomase) (Cyclophilin C).
 GN Cyp-6 OR P42639.2.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Pelodierinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX STRAIN-Bristol N2;
 RX MEDLINE=96276416; PubMed=8694762;
 RA Page A.P., Macniven K., Hengartner M.O.;
 RT "Cloning and biochemical characterization of the cyclophilin
 RT homologues from the free-living nematode *Caenorhabditis elegans*.";
 RL Biochem. J. 317:179-185(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX STRAIN-Bristol N2;
 RA Taich A.;
 RL Submitted (MAY-1994) to the EMBL/Genbank/DBJ databases.
 CC -1- FUNCTION: PPIases accelerate the folding of proteins. It catalyzes
 CC the cis-trans isomerization of proline imidic peptide bonds in
 CC oligopeptides.
 CC -1- CATALYTIC ACTIVITY: Peptidylproline (omega-180) - peptidylproline
 CC (omega-0).
 CC -1- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY.
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DR EMBL: U27354; AAC47124.1; -
 DR EMBL: U00051; AAA91355.1; -
 DR HSSP: P23284; ICYN.
 DR WormPep: F4269.2; CE01301.
 DR InterPro: IPR002130; CSA_PPIase.
 DR Pfam: PF00160; PRO_Isoomerase; 1.

DR PRINTS: PS00153; CSAPPISMRASE.
 DR PROSITE: PS00170; CSA_PPIASE.1; 1.
 DR PROSITE: PS50072; CSA_PPIASE.2; 1.
 KW Isoomerase; Rotomase; Multigene family; Signal.
 FT SIGNAL 1 16
 FT CHAIN 17 201
 FT CARBOHYD 130 130
 SQ SEQUENCE 201 AA; 21864 MW; 084C5762917F958B CRC64;
 N-LINKED (GLCNAC...) (POTENTIAL).

Query Match 7.7%; Score 16; DB 1; Length 201;
 Best Local Similarity 100.0%; Pred. No. 2.1e-07;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 92 FMIQGDFTRDGTGG 107
 Db 82 FMIQGDFTRDGTGG 97
 |||||

RESULT 9
 CYPC_HUMAN STANDARD; PRT; 212 AA.
 ID CYPC_HUMAN
 AC P45877;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Peptidyl-prolyl cis-trans isomerase C (EC 5.2.1.8) (PPIase) (Rotomase)
 DE (Cyclophilin C).
 GN PPIC OR CYPC.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94304830; PubMed=8031755;
 RA Schneider H., Charara N., Schmitz R., Wehrli S., Mikol V.,
 RA Zurini M.G., Quesnaux V.F., Moyva N.R.;
 RT "Human cyclophilin C: primary structure, tissue distribution, and
 RT determination of binding specificity for cyclosporins.";
 RL Biochemistry 33:8218-8224(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX TISSUE=Uterus;
 RA Strausberg R.;
 RL Submitted (FEB-2001) to the EMBL/Genbank/DBJ databases.
 CC -1- FUNCTION: PPIases accelerate the folding of proteins. It catalyzes
 CC the cis-trans isomerization of proline imidic peptide bonds in
 CC oligopeptides.
 CC -1- CATALYTIC ACTIVITY: Peptidylproline (omega-180) - peptidylproline
 CC (omega-0).
 CC -1- ENZYME REGULATION: CYCLOSPORIN A (CSA) INHIBITS CYPC.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY.
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DR EMBL: S71018; AAB31350.1; -
 DR EMBL: BC002678; AAH02678.1; -
 DR HSSP: P05092; ZPMC.
 DR Genew: HGNC:9256; PPIC.
 DR MIM: 123842; -
 DR InterPro: IPR002130; CSA_PPIase.
 DR Pfam: PF00160; PRO_Isoomerase; 1.
 DR PRINTS: PS00153; CSAPPISMRASE.
 DR PROSITE: PS00170; CSA_PPIASE.1; 1.
 DR PROSITE: PS50072; CSA_PPIASE.2; 1.
 KW Cyclosporin; Isoomerase; Rotomase; Multigene family.

SQ	SEQUENCE	212 AA;	22763 MW;	6F3DB547A2AE581B CRC64;
OY	Query Match	7.7%;	Score 16;	DB 1; Length 212;
Db	Best Local Similarity	100.0%;	Pred. No. 2,2e-07;	Mismatches 0;
Matches	16;	Conservative	0;	Mismatches 0; Indels 0; Gaps 0;
OY	83 SKFRVAKDFMIOGSD 98			
Db	85 SKFRVAKDFMIOGSD 100			
RESULT 10	CYC_MOUSE	STANDARD:	PRT:	212 AA.
ID	CYC_MOUSE			
AC	P30412;			
DT	01-APR-1993 (rel. 25; Created)			
DT	01-APR-1993 (rel. 25; Last sequence update)			
DT	15-JUN-2002 (rel. 41; Last annotation update)			
DE	Peptidyl-prolyl cis-trans isomerase C (EC 5.2.1.8) (PPIase) (Rotamase)			
GN	(Cyclophilin C).			
OS	PPIC OR CYC.			
OC	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	MEDLINE=91347379; PubMed=1652374;			
RA	Friedman J., Weissman I.L.;			
RT	"Two cytoplasmic candidates for immunophilin action are revealed by affinity for a new cyclophilin: one in the presence and one in the absence of CsA.";			
RL	Cell 66:799-806(1991).			
CC	-1- FUNCTION: Pripases accelerate the folding of proteins. It catalyzes the cis-trans isomerization of proline imidic peptide bonds in oligopeptides.			
CC	-1- CATALYTIC ACTIVITY: Peptidylproline (omega-180) = peptidylproline (omega-0).			
CC	-1- ENZYME REGULATION: CYCLOSPORIN A (CSA) INHIBITS CYPC.			
CC	-1- SUBCELLULAR LOCATION: Cytoplasmic.			
CC	-1- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY.			
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DR	EMBL; M74227; AAA37511.1; .			
DR	PIR; A40047; A40047.			
DR	HSSP; P05092; 2RMC.			
DR	MGI; MGI:97751; Ppic.			
DR	InterPro; IPRO02130; CSA_PPIase.			
DR	Pfam; PF00160; pro_isomerase_1.			
DR	PRINTS; PR00153; CSAPPISMRASE.			
DR	PROSITE; PS00170; CSA_PPIASE_1; 1.			
DR	PROSITE; PS50072; CSA_PPIASE_2; 1.			
KW	Cyclosporin; Isomerase; Rotamase; Multigene family.			
FT	CONFLICT 212 AA; 22794 MW; C99ETAA5D0FF04B6 CRC64;			
SO	SEQUENCE			
Query Match	7.7%;	Score 16;	DB 1; Length 212;	
Best Local Similarity	100.0%;	Pred. No. 2,2e-07;		
Matches	16;	Conservative	0;	Mismatches 0; Indels 0; Gaps 0;
OY	85 FHRVAKDFMIOGSDFT 100			
Db	87 FHRVAKDFMIOGSDFT 102			
RESULT 11	CYP7_CABEL			
ID	CYP7_CABEL	STANDARD:	PRT:	171 AA.
AC	P52015;			
DT	01-OCT-1996 (rel. 34; Created)			
DT	16-OCT-2001 (rel. 40; Last sequence update)			
DT	15-JUN-2002 (rel. 41; Last annotation update)			
DE	Peptidyl-prolyl cis-trans isomerase 7 (EC 5.2.1.8) (PPIase) (Rotamase)			
GN	(Cyclophilin-7).			
OS	CYP-7 OR Y75B12B.2.			
OS	Caenorhabditis elegans.			
OC	Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditiida; Rhabditoidea;			
OC	Rhabditidae; Pelodierinae; Caenorhabditis.			
OX	NCBI_TaxID=6239;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=Bristol N2;			
RC	MEDLINE=96276416; PubMed=8694762;			
RA	Page A.P., Macniven K., Hengartner M.O.;			
RT	"Cloning and biochemical characterization of the cyclophilin RT homologues from the free-living nematode Caenorhabditis elegans.";			
RL	Biochem. J. 317:179-185(1996).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=Bristol N2;			
RA	White S.;			
RL	Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.			
RN	[3]			
RP	SEQUENCE OF 1-13.			
RC	STRAIN=Bristol N2;			
RC	MEDLINE=97295299; PubMed=9150941;			
RA	Bini L., Heid H., Libertori S., Geler G., Pallini V., Zwilling R.;			
RT	"Two-dimensional gel electrophoresis of Caenorhabditis elegans RT homogenates and identification of protein spots by microsequencing.";			
RL	Electrophoresis 18:557-562(1997).			
CC	-1- FUNCTION: Pripases accelerate the folding of proteins. It catalyzes the cis-trans isomerization of proline imidic peptide bonds in oligopeptides.			
CC	-1- CATALYTIC ACTIVITY: Peptidylproline (omega-180) = peptidylproline (omega-0).			
CC	-1- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY.			
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DR	EMBL; U27559; AAC47125.1; .			
DR	AL032663; CAAT1760.1; .			
DR	HSSP; P05092; 1CWL.			
DR	Siens-2DPAGE; P52015; .			
DR	Wormpep; Y75B12B.2; CE20371.			
DR	InterPro; IPRO02130; CSA_PPIase.			

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ID  CYPB.CAEEL  STANDARD:  PRT:  183 AA.
AC  P52018:
DT  01-OCT-1996 (Rel. 34, Created)
DT  01-OCT-1996 (Rel. 34, Last sequence update)
DT  15-JUN-2002 (Rel. 41, Last annotation update)
DE  Peptidyl-prolyl cis-trans isomerase II (EC 5.2.1.8) (PPIase)
DE  (Rotamase) (Cyclophilin-11).
GN  CYP-11 OR T01B7.4.
OS  Caenorhabditis elegans.
OC  Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC  Rhabditidae; Peloderinae; Caenorhabditis.
OX  NCBI_TaxID=6239;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN-Bristol N2;
RX  MEDLINE=96276416; PubMed=8694762;
RA  Page A.P., Macniven K., Bengtner M.O.;
RT  "Cloning and biochemical characterization of the cyclophilin
RT  homologues from the free-living nematode Caenorhabditis elegans.";
RL  Biochem. J. 317:179-185(1996).
RN  [2]
RP  SEQUENCE FROM N.A.
RC  STRAIN-Bristol N2;
RA  Sims M.;
RT  Submitted (OCT-1995) to the EMBL/GenBank/DBJ databases.
CC  -1- FUNCTION: PPIases accelerate the folding of proteins. It catalyzes
CC  the cis-trans isomerization of proline imidic peptide bonds in
CC  oligopeptides.
CC  -1- CATALYTIC ACTIVITY: Peptidylproline (omega-180) - peptidylproline
CC  (omega-0).
CC  -1- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY.
CC  -----
CC  This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC  or send an email to license@isb-sib.ch).
CC  -----
DR  EMBL: U34955; AAC47115.1; -
DR  EMBL: Z66499; CAA91297.1; -
DR  HSSP: P05092; 2CPL.
DR  WormPep: T01B7.4; CE03588.
DR  InterPro: IPR002130; CSA_PPIase.
DR  Pfam: PF00160; PRO_Isomerase.1.
DR  PRINTS: PR00153; CSAPPISMRASE.
DR  PROSITE: PS00170; CSA_PPIASE.1; 1.
DR  PROSITE: PS50072; CSA_PPIASE.2; 1.
KM  Isomerase; Rotamase; Multigene family.
SQ  SEQUENCE 183 AA; 20193 MW; 23549C922828C533 CRC64;

Query Match 7.2%; Score 15; DB 1; Length 183;
Best Local Similarity 100.0%; Pred. No. 1.6e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 85 FRRVTKDFMIOGDF 99
DB 71 FRRVTKDFMIOGDF 85

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OX  NCBI_TaxID=160;
RN  [1]
RP  SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RX  MEDLINE=97461344; PubMed=9317025.
RA  Shevchenko D.V., Aktis D.R., Robinson E.J., Li M., Shevchenko O.V.,
RA  Radolf J.D.;
RT  "Identification of homologs for thioredoxin, peptidyl prolyl cis-trans
RT  isomerase, and glycerophosphodiester phosphodiesterase in outer
RT  membrane fractions from Treponema pallidum, the syphilis spirochete.";
RL  Infect. Immun. 65:4179-4189(1997).
RN  [2]
RP  SEQUENCE FROM N.A.
RC  STRAIN-Nichols;
RX  MEDLINE=98332770; PubMed=965876;
RA  Fraser C.M., Norris S.J., Weinstock G.M., White O., Sutton G.G.,
RA  Dodson R., Gwin M., Hickey E.K., Clayton R., Ketchum K.A.,
RA  Sodergren E., Hardham J.M., McLeod M.P., Salzberg S., Peterson J.,
RA  Khalak H., Richardson D., Howell J.K., Chidambaram M., Uterback T.,
RA  McDonald L., Artach P., Bowman C., Cotton M.D., Fujii C., Garland S.,
RA  Hatch B., Horst K., Roberts K., Sandusky M., Weidman J., Smith H.O.,
RA  Venter J.C.;
RT  "Complete genome sequence of Treponema pallidum, the syphilis
RT  spirochete.";
RL  Science 281:375-388(1998).
CC  -1- FUNCTION: PPIases accelerate the folding of proteins. It catalyzes
CC  the cis-trans isomerization of proline imidic peptide bonds in
CC  oligopeptides (By similarity).
CC  -1- CATALYTIC ACTIVITY: Peptidylproline (omega-180) - peptidylproline
CC  (omega-0).
CC  -1- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY.
CC  -----
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CC  use by non-profit institutions as long as its content is in no way
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CC  entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC  or send an email to license@isb-sib.ch).
CC  -----
DR  EMBL: U97573; AAC08055.1; -
DR  EMBL: AE001263; AAC05904.1; -
DR  HSSP: P05092; 2RMC.
DR  TIGR: TP0947; -
DR  InterPro: IPR002130; CSA_PPIase.
DR  Pfam: PF00160; PRO_Isomerase.1.
DR  PRINTS: PR00153; CSAPPISMRASE.
DR  PROSITE: PS00170; CSA_PPIASE.1; 1.
DR  PROSITE: PS50072; CSA_PPIASE.2; 1.
KM  Isomerase; Rotamase; Complete proteome.
SQ  SEQUENCE 215 AA; 23272 MW; CCA1589C1F5A6D0B CRC64;

Query Match 6.7%; Score 14; DB 1; Length 215;
Best Local Similarity 100.0%; Pred. No. 1.5e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 85 FRRVTKDFMIOGDF 98
DB 89 FRRVTKDFMIOGDF 102

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RESULT 13
PPIB_TREPA  STANDARD:  PRT:  215 AA.
AC  O66105:
DT  15-DEC-1998 (Rel. 37, Created)
DT  15-DEC-1998 (Rel. 37, Last sequence update)
DT  15-JUN-2002 (Rel. 41, Last annotation update)
DE  Probable peptidyl-prolyl cis-trans isomerase (EC 5.2.1.8) (PPIase)
DE  (Rotamase).
GN  PPIB OR PPI OR TP0947.
OS  Treponema pallidum.
OC  Bacteria; Spirochaetales; Spirochaetaceae; Treponema.

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RESULT 14
CYPB_ALICE  STANDARD:  PRT:  150 AA.
AC  P34887:
DT  01-FEB-1994 (Rel. 28, Created)
DT  01-FEB-1994 (Rel. 28, Last sequence update)
DT  15-JUN-2002 (Rel. 41, Last annotation update)
DE  Peptidyl-prolyl cis-trans isomerase (EC 5.2.1.8) (PPIase) (Rotamase)
DE  (Cyclophilin) (Cyclosporin A-binding protein).
GN  CYP.
OS  Allium cepa (Onion).
OC  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC  Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Alliaceae;

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CC Allium.
 RX NCBI_TaxID=4679;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Clark S.A.;
 RL Submitted (XXXX-1993) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Pripases accelerate the folding of proteins. It catalyzes
 the cis-trans isomerization of proline imidic peptide bonds in
 oligopeptides.
 CC -1- CATALYTIC ACTIVITY: Peptidylproline (omega-180) - peptidylproline
 (omega-0).
 CC -1- ENZYME REGULATION: BINDS CYCLOSPORIN A (CSA). CSA MEDIATES SOME
 OF ITS EFFECTS VIA AN INHIBITORY ACTION ON PPIASE.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC -1- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY.
 CC
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 CC
 CC EMBL: L13365; AAA2642.1; -.
 DR HSP: P05092; 2CPL.
 DR InterPro: IPR002130; CSA_PPIase.
 DR Pfam: PF00160; pro_isomerase; 1.
 DR PRINTS: PR00153; CSAPPISRMASE.
 DR PROSITE: PS00170; CSA_PPIASE_1; 1.
 DR PROSITE: PS50072; CSA_PPIASE_2; 1.
 KW Cyclosporin; Isomerase; Rotamase; Multigene family.
 SO SEQUENCE 150 AA; 16033 MW; 9223D16840F7E241 CRC64;

Query Match 6.2%; Score 13; DB 1; Length 150;
 Best Local Similarity 100.0%; Pred. No. 9.6e-05;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 150 KTAWLDDGKHVFC 162
 |||||
 Db 103 KTAWLDDGKHVFC 115

RESULT 15
 CYPB_YEAST STANDARD; PRT; 205 AA.
 ID CYPB_YEAST STANDARD; PRT; 205 AA.
 AC P23285;
 DT 01-NOV-1991 (Rel. 20, Created)
 DT 01-NOV-1991 (Rel. 20, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Peptidyl-prolyl cis-trans isomerase B precursor (EC 5.2.1.8) (PPIase)
 GN (Rotamase) (Cyclophilin B) (Cyclophilin-related protein).
 OS CYP2 OR CYP2 OR SCC2 OR CRG OR YHR057C.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 CC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
 CX NCBI_TaxID=4932;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90221907; PubMed=2183199;
 RA Koser P., Sylvestre D., Liyi G.P., Bergsma D.J.;
 RT "A second cyclophilin-related gene in Saccharomyces cerevisiae.";
 RL Nucleic Acids Res. 18:1643-1643(1990).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX STRAIN=5288C / AB972;
 MEDLINE=94378003; PubMed=8091229;
 RA Johnston M., Andrews S., Brinkman R., Cooper J., Ding H., Dover J.,
 Du Z., Favellio A., Fulton L., Gatlung S., Gelsel C., Kirsten J.,
 Kucaba T., Hillier L., Jler M., Johnston L., Langston Y.,
 Lacroelle P., Louis E.J., Macri C., Mardis E., Meneses S., Mouser L.,
 Nhan M., Rifkin L., Riles L., St Peter H., Trevasakis E., Vaughan K.,
 Vignati D., Wilcox L., Wohlman P., Waterston R., Wilson R.,

RA Vaudin M.;
 RT "Complete nucleotide sequence of Saccharomyces cerevisiae chromosome
 VII.";
 RL Science 265:2077-2082(1994).
 RN [3]
 RP CHARACTERIZATION.
 RX MEDLINE=92104509; PubMed=1761234;
 RA Koser P., Bergsma D.J., Cafferty R., Eng W.-K., McLaughlin R.M.,
 RA Ferrara A., Silverman C., Kasyan K., Bossard M.J., Johnson R.K.,
 RA Porter T.G., Levy M.A., Liyi G.P.;
 RT "The CYP2 gene of Saccharomyces cerevisiae encodes a cyclosporin A-
 sensitive peptidyl-prolyl cis-trans isomerase with an N-terminal
 signal sequence.";
 RL Gene 108:73-80(1991).
 CC -1- FUNCTION: Pripases accelerate the folding of proteins. It catalyzes
 the cis-trans isomerization of proline imidic peptide bonds in
 oligopeptides.
 CC -1- CATALYTIC ACTIVITY: Peptidylproline (omega-180) - peptidylproline
 (omega-0).
 CC -1- ENZYME REGULATION: CYCLOSPORIN A (CSA) INHIBITS CYPB.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY.
 CC
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 CC
 CC EMBL: X51497; CAA35865.1; ALT_SEQ.
 DR EMBL: U00061; AAB68386.1; -.
 DR PIR: S12324; S12324.
 DR PIR: S46707; S46707.
 DR HSP: P23284; 1CYN.
 DR SGD: S0001099; CYP2.
 DR InterPro: IPR002130; CSA_PPIase.
 DR Pfam: PF00160; pro_isomerase; 1.
 DR PRINTS: PR00153; CSAPPISRMASE.
 DR PROSITE: PS00170; CSA_PPIASE_1; 1.
 DR PROSITE: PS50072; CSA_PPIASE_2; 1.
 KW Cyclosporin; Isomerase; Rotamase; Signal; Multigene family.
 FT SIGNAL 1 20
 FT CHAIN 21 205
 FT OR 34 (POTENTIAL).
 SO SEQUENCE 205 AA; 22769 MW; 616EAB434837A6D CRC64;

Query Match 6.2%; Score 13; DB 1; Length 205;
 Best Local Similarity 100.0%; Pred. No. 0.00012;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 136 GKDTNGSQFPTT 148
 |||||
 Db 137 GKDTNGSQFPTT 149

Search completed: April 10, 2003, 11:54:34
 Job time : 12 secs